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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                   - nucleic search, using frame_plus_p2n model
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                                   GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHis
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Dolichos.
I (bases I to 1608)
Etzler,M.B., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B. and
Murphy,J.B.
A nod factor binding lectin with apyrase activity from legume roots
Proc.
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INPOGELITSTAVITPIGASSGRYVHYNFDQNIDLIHGONDLEFTKKITGGLSSYDDKP
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KGSGQKNLVVTSAFYTKSSEVGFVTPPNSKNRPLDFFETAAKQACSLTFEEAKSTFPNV
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CA 95616, USA
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Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B.
1608 bp mRNA linear PLN :
Dolichos biflorus nod factor binding lectin-nuclectide
phosphohydrolase (LNP) mRNA, complete cds.
AF139807.1 GI:486R17A
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/product="nod factor binding lectin-nucleotide
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/db_xref="GI:4868375"
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Direct Submission
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421 GlnGlulleThrValAlaGluGlylleGluTyrGlnAspAlaIleValGluTh	z £	Unclassified.  1 (bases 1 to 1643) Etaler,M.E. and Murphy, J.B. Nod factor binding protein from legume Patent: US 646716-A 1 15-OCT-2002; Location/Qualifiers 1. 1643 /organism="unknown" /mol_type="genomic DNA"	Alignment Scores: Pred. No.: Score: Score: Score: Anilarity: Descrent Similarity: Descrent Similarity: Descrent Similarity: Descrent Similarity: Descrent Similarity: Description Matches: Description	1 MetasnTrpValTrpProLysThrLysSerMetSerPheLeuLeuLleThrPheLeu			121 ProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgleuCluGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgleuCluGluGluGluChill
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1395   ACAAAAAATGGAATTGAAAGACCAAATAAAATATGGCCCTTATCGTAAAAATGTTT   1454     133	CATTICCTTAIGTIATTAACTAGGCTTTCAATGTCTTAACTTTCGTTTTCTCTCATGTTGValargGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSer	172 ValileAspGlyThrGlnGluGlySerTyrLeuTrpVal	184 184  1874 ACCTAGGACATTCATCTATTTAAAATAATTTATTGCAAAATAATACTATTTTTTAATTA 1933  184		GTGTGTGGTGACATGCCCATACCCCATATGGACAATTACTGACATGCCATACCGATATAT	184		2354 AICACGACGAIAIAATTIGIAIAAGIAAITTAAAITCACTAITCATTITAITIGIIG 2413 184	184 184 2474 AAGAAAGAAGCAATGAAATTAAAAGTGGATCAAACCATGAGGATATGTTTCAAAAG 2533
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SOURCE ORGANISM Unknown. ORGANISM Unknown. Unclassified. 1 (bases 1 to 6265) AUTHORS Btler,M.E. and Murphy,J.B. AUTHORS Btler,M.E. and Murphy,J.B. TITLE Nod factor binding protein from legume roots JUTHOR Btler. US 6465116-A 315-OCT-2002; FEATURES 1. 6262   Location/Qualifiers   Locati	Alignment Scores: 2.05e-142 Length: 6265  Pred. No.: 2.05e-142 Length: 6265  Score: 1741.00 Matches: 461  Percent Similarity: 29.01\$ Conservative: 0  Dest Local Similarity: 29.01\$ Mismatches: 1  Ouery Match: 6 Gaps: 8  Indels: 8	1 MetAsnTrpValTrpProLysTh 1 MetAsnTrpValTrpProLysTh 675 ATGATTGGGTGTGGCCAAAGAC 21 LeuPheSerLeuProLysLeuSe 7.35 CTCTTCTCTCAAGACTTTTCTTCTCAAGACTTTTCTTCTCAAGACTTTTCTTCTCAAGACTTTTTTTT	41 HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla 41 HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla 795 CATCGTAAGATACTTCCCAACCAGGAACTCCTTACGCTGTCATCTTGATGCT 61 GlySerSerGlySerArgValHisValPheAspGlhAsnLeuAspLeuLeuHis	Db 855 GGTAGCTCTGGGAGTCGTCCATGTTTTGACCAGAACTTAGATCTCTGCAC 914  Qy 81 IleGlyAsnAspLeuGluPheThrLySLys	QY         91	115 GlualaGluaspValValProGluGluLeuHisProLysThrProLeuLysLu 	5 AGTATTTCTCATCTCTACTTTTGCCACAGATTAATATGTCACACTTTTACATGAAACATG 3	TGATGGA	Db 1335 ACAGAAGAAAGCAATATCAAGAGACACAAAACACACACTTTGATGAGCTCTATTTAA 1394 Qy 133133

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AUTHORS Day,R.B., McAlvin,C.B., Loh,J.T., Fink,S.E., Denny,R.L., Dunlap,J., Young,N.D. and Stacey,G. TITLE Direct Submission JOURNAL Submitted (21-NOV-1999) Microbiology, The University of Tennessee, M469 Wallers Life Science Building, Knoxville, TN 37996-0845, USA Location/Qualifiers    1.1463 Wallers   Location/Qualifiers     2.1463 Wallers   Location/Qualifiers     3.1476="MarkNa"     3.1421   Codon Start = 1     2.1421   Codon Start = 1     3.1421   Codon Start = 1     4.152137"   Codon Start = 1     4.152137"   Codon Start = 1     5.1421   Codon Start = 1     6.11225137"   Codon Start = 1     7.1421   Codon Start		Db 44.7 Trisgaagisciatortsaaagaatartriscaagisciatortsaagaa 506   Qy
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Nod factor binding protein from legume
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                                                                                                                                                                                       TACGATGGGACCTACACATATTCAGGAGCAGACTATAAGGCCTTCGCTCCCATTTCTGGC
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Unclassified. 1 (bases 1 to 1489) Etzler, M.E. and Murphy, J.B.

patent GI:27282688

Sequence 13 from AR237865 AR237865.1

Unknown. Unknown

> ORGANISM REFERENCE AUTHORS

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319
68
71
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Mismatches:
Indels:
                                                                   Matches:
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1684.00
83.05%
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Best Local Similarity:
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
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853 GCTGGCTTTGATGGGGCATATACATATTCCGGAGCAGAGTATAAAGGTCTCGGCCCCAGCT 912
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                                                                                                         LeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleVal
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                                                                                                                                                                                                                     GlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe
                                                                                                                                                                                                                                                                                                                                                                                                                    LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly
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    1489
/organism="Lotus corniculatus var. japonicus"

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Lotus japonicus nod factor binding lectin-nucleotide phosphohydrolase (LNP) mRNA, complete cds.
AF156780
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Roberts, N.J., Brigham, J., Wu,
Phillips, D.A. and Etzler, M.E.
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Expression of the Apyrase-Like APYI Genes in Roots of Medicago truncatula Is Induced Rapidly and Transiently by Stress and Not Sinorhizobium meliloti or Nod Factors Plant Physiol. 131 (3), 1124-1136 (2003)
                                                                                Cullinors, V. v. and Niebel, A. Direct Submission Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
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/gene="APY1;4"
21. .1388
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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            LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer
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|GCTGGCTTTGATGGGGCATATACATATTCCGGAGCAGAGTATAAGGTCTCGGCCCCAGCT
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Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V.
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              AlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSer
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Unclassified.

I (bases 1 to 1458)

RS Etzler,M.E. and Murphy,J.B.

Nod factor binding protein from legume roc

Location/Qualifiers

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Matches:
Conservative:
Mismatches:
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1458 bp US 6465716

AR237864 Seguence 8 from patent <sup>1</sup> AR237864 AR237864.1 GI:27282687

AR237864 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

RESULT

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Percent Similarity:
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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Submitted (07-UTN-1999) Molecular and Cellular Biology, University
of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA
Location/Qualifiers
GAICTCTAIGITCATAGITACTIGCGITTIGGCAAAGAAGCAACTCGAGCACAGGITTIG 783
                         LysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArg
                                                                                                                                                                                      PhedlydlylleTrpAspGlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSer
                                     AATGCAACTAATGGATCTGCTAACCCTTGCATTTTACCTGGATTTAATGGGACCTTTACA
                                                                                            304 AAAGAAATAATTCTTAAAGTTCTTAAAGTAAATGATCCATGTCCCTATCCGAGTTGCACT
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                                                                             TyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCys
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A Nod factor-binding lectin is a member of a distinct class apyrases that may be unique to the legumes
Mol. Gen. Genet. 262 (2), 261-267 (1999)
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Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.
Phillips,D.A. and Etzler,M.E.
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YAVIFDAGSTGTRVHYYHFQNLDLLHIGNDIEFVDKIKPGLSAYGDNPEQAAKSLIP
LLEBEBDVVBEDLHPKTPIELGATAGELLNGDABAGKILGAFURMFSNRSTLMVQRDA
VSITDGTQEGSYMWYUNYVLGNLGKSFTKSVGYLDLGGGSGYQMTYAVSKKTAKNAPK
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TYSGYBYKARSPSSGSNFDDCKEIILKVLKYNDPCPYPSCTPGGIWNGGGGSGQKKLF
TYSGYBYKARSPSSGSNFDDCKEIILKVLKYNDPCPYPSCTPGGIWNGGGGSGQKKLF
VCARATALBDVGWVEPNKPNSILHPVDFEIEAKRACALNFEDVKSTYPRLTDAKRPY
VCMDLLYQHVLLVHGFGLGFRKEITVGGGLQYQNSVVBAAMPLGTAVBAISALPRFKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LeuSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AAACAAGAAACCTTAACCCTCTACCCTGTCATATTTGATGCTGGTAGCACTGGTACTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 GTCCATGTTTACCATTTTGATCAGAACTTAGATCTACTTCACATTGGCAATGATATTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 AAATCTCTCATTCCACTTTTGGAGGAAGCAGAAGATGTGGTTCCTGAGGATCTGCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg
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                                                                                                                                                                                                    product="nod factor binding lectin-nucleotide
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                /protein_id="AAF00611.1"
/db_xref="G1:6006799"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-657-631-2 (1-462) x AF156782 (1-1460)
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                                                                                                                                                                                                                         phosphohydrolase
                                                                                                                                                                               codon_start=1
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1654.50
82.75%
67.03%
                                                                                    /gene="LNP"
15. .1382
                                                                                                                                gene="LNP"
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YPLLVDFNILYBYVANDLYQYVLLVDGFGLDPLQEITAGKQIEYQDSLVEAANPLGNN
VAAISSLPKFERLMYFI"
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2 (bases 1 to 1486)
Cullimore, J.V. and Niebel, A.
Direct Submission
Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan 31326, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp
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Mismatches:
Indels:
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                                                                                                                                                                    /mol_type="mRNA"
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                                                                                                            Location/Qualifiers
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7. .1410
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Best Local Similarity:
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                     666 AAAGTTGCTGATGGAGAGGATCCATATATTAAGAAGCTTGTGCTCAAGGAAAGCAATAT
                                                                                                                                                                                                                             267 LysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArg
                                                                                                                                                                                                                                                                                                                                                                          ArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThr
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                                                                                 LysProProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr
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1 (bases 1 to 1500)
Navarro-Gochicoa, M.T., Camut, S., Niebel, A. and Cullimore, J.V.
Expression of the Apyrase-Like APYI Genes in Roots of Medicago Sinorhizobium meliloti or Nod Factors
Plant Physiol. 131 (3), 1124-1136 (2003)
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                                                                                                                                                                                                                                             Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
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/organism="Medicago truncatula"
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Cullimore, J.V. and Niebel, A. Direct Submission
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/codon_start=1
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                          LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu
                                                                                                     TCAATGTTCAACCTGATGCAGTTTCTATTATTGATGAACCCAAGAAGGTTCTTATCTC
                                                                                TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
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1348 TGCATGGCCACTAGGCAATGCTGTAGAAGCCATATCATCGTTACCTAAATTTGAAAAATT 1407
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Cohn,J., Ramu,S., Uhm,T., Nam,Y.W., Kim,D.J., Penmetsa,V., Wood,T.,
Cohn,J., Denny,R., Young,N. and Stacey,G.
Direct Submission
Submitted (17-JUL-2000) Microbiology, University of Tennessee, M409
                                                                                                                                                                                                                                                                                                                                                                                               Cohn,J.R., Uhm,T., Ramu,S., Nam,Y.W., Kim,D.J., Penmetsa,R.V., Wood,T.C., Denny,R.L., Young,N.D., Cook,D.R. and Stacey,G. Differential regulation of a family of apyrase genes from Medicago
                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/note="nucleotide phosphohydrolase; Mtapy1"
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Medicago truncatula putative apyrase (apy1) mRNA,
AF288132
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Arganism="Medicago truncatula"
mol type="mRNA"
db_xref="taxon:3880"
map="linkage group 7"
fissue_type="roots"
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/gene="apy1"
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Shibata,K., Morita,Y., Abe,S., Stankovic,B. and Davies,E.
Apyrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of
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TITAATAAATGCAAAAACACAATTCGTAAGGCTCTTAAGTTGAACTATCCTTGTCCATAT
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                                                                                                                                                                                                                                                                                               TrpProLeuGlyThrAlalleGluAlalleSerSerLeuProLysPheAsnArgLeuMet
      GlyLysLysLyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArg
                                     728 ggaataccatatgatctctatgttcacagttacttacacttcggtagagaagcatctcga
                                                                        263 VallysilePhelysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGlu
                                                                                                       GCAGAGATTTTGAAGCTCACTCCTCGTTCTCCTAACCCTTGCCTTTTAGCTGGATTTAAT
                                                                                                                                        AsplleTyrargTyrSerGlyGluSerTyrAsnlleTyrGlyProThrSerGlyAlaAsn
                                                                                                                                                                       848 GGAATCTATACATATTCAGGAGAGAGTTTTAAGGCAACTGCTTACACTTCTGGTGCAAAC
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AVVEDAGSTGER HYYTHENONLDLIHIGKGVERYNKI TPGLESSYANNEDGAKKELIEU
LEGAEDVVEDDLOPKTPVKLGATGGLRLINGDASEKILGSYRDMLSNRSTENVOPDAV
SLEGAEDVVEDDLOPKTPVKLGATGGLRLINGDASEKILGSYRDMLSNRSTENVOPDAV
SLIDGTOEGSYLMVYNYALGHLGKKYTKTVGYTDLGGGGSVQPANAVSKKTANARAV
ADGDDPYIKKVVLKGIPYDLYVHSYLHFGRRASRAEILKLIFRSPNPCLLAGFNGIYT
SKGEBFRATATYSGANPRKKNNITKALKLINYPCPYONCTFGGINNGGGGNGCKNLFA
SSSFFYLPEDTGWYDASTPNFILRPVDIETKAKEACALNFEDAKSTYPFLDKKNVASY
VCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEBANFERR
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Conservative:
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Indels:
/product="S-type apyras"
/protein_id="BAB40230.1"
/db_xref="G1:13488667"
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                       488 TICAACGTICAACGAGGGGAGTTTCTATAATTGATGGAACCCAAGAAGGTTCTTATCTA
                                                                                                                           ValileAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAla
                                                                                                                                                                                                                                                                                                                              GCAGAGATTITGAAGCICACTCCTCGTICTCCTAACCCTIGCCTTTAGCTGGATTITAGT
      LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu
                                                                  TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
                                                                                              548 regereacharacrargearregeaarrragesaaaagracacaaaaacagrrega
                                                                                                                                                       608 GTAATAGATCTTGGAGGTGGATCAGTTCAAATGGCGTATGCAGTATCAAAGAAAACTGCT
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|28 AAGATTTTCCTAAAACAAGAGAAATTTCCTCTTACGCTGTCGTATTCGATGCTGGTAGC
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Fax:+81-89-946-9853)
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Matches:
Conservative:
Mismatches:
Indels:
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       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
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Submitted (10-SEP-2001) Tomonori Shiraishi, Okayama Univers
1-1-1 Tsushima naka, Okayama city, Okayama 700-8530, Japan
(E-mail:tomoshiracc.okayama-u.ac.jp, Tel:81-86-251-8311,
                                                                              and
                                                                            Toyoda, K., Ichinose, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name="nucleoside triphosphatase"
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Shiraishi,T.
Characterization of Pea Cell Wall-bound Apyrase
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Aaf31693 Human CD3
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 NBP46 (root lectin) cDNA
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                OM protein - nucleic search, using frame_plus_p2n model
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, replents, of NBP46 can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
                                                                 New polynucleotides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
                                                                                                                                                  Claim 3; Page 42; 57pp; English.
WPI; 1999-167136/14.
                          P-PSDB; AAW85684
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Sequence 1643 BP; 505 A; 317 C; 347 G; 474 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/mucleotide promoter operably linked to a heterologous LNP (lectin/mucleotide) in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polymucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the bolichos biflorus lectin/nucleotide phosphohydrloase (LNP) that can be used to modulate mycorrhizal infection in plants
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                                                                      /note= "Lectin/nucleotide phosphohydrolase"
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iocation/Qualifiers
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                                                   'product= "LNP"
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                                                                                                                                                                                                                                     The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening when need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
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                                                                                                                                                                                      New polynuclectides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
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Best Local Similarity:
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                        NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen; so.
             ProLeuGlyThrAlaileGluAlaileSerSerLeuProLysPheAsnArgLeuMetTyr
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                           NBP46 (root lectin) genomic DNA.
                                                                                                                 AAX08523 standard; DNA; 6265 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide promoter operably linked to a heterologous LNP (lectin/nucleotide phosphohydrolase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the colynucleotide), resulting in increase dutake of nutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Medicago sativa lectin/nucleotide phosphohydrloase (LNP) that can be used to modulate mycorrhizal infection in plants
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                                                                                                                                                                             LNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating mycorhizal infection, useful for improving plant growth, transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
                                                                                                                                                                      DNA encoding Medicago sativa lectin/nucleotide phosphohydrolase,
                                                                                                                                                                                               Lectin/nucleotide phosphohyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein, nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth; plant development; antisense technology; gene; ds.
                                                                                                                                                                                                                                                                                                                                                              note= "Lectin/nucleotide phosphohydrolase"
                                                                                                                                                                                                                                                                                                                                                                     /partial
/note= "No start or stop codon given"
/transl_except= (pos:22. .24, aa:Xaa)
/transl_except= (pos:1411. .1413, aa:Xaa)
/transl_except= (pos:1453. .1455, aa:Xaa)
/note= "Xaa= Stop codon"
                             5440
 LysPheAsnArgLeuMetTyrPhelle 462
                            5414 AAATTTAATCGTCTAATGTATTTATC
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 35-37; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                'product= "LNP"
                                                                                   DNA; 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000; 2000US-00657631.
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                                                                                                                                            (first entry)
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P-PSDB; AAU78820.
                                                                                   ABK11100 standard;
                                                                                                                                                                                                                                                                       Medicago sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200220725-A2
                                                                                                                                           18-JUN-2002
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454
                                                                                                              ABK11100;
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33 GIGTICATGITAATGCCTGCTATCTTCCTCCCAATATCTCGGAAACAACATTCTCATG 132
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                                                                                                                                                                                                                                                                                                                                                                                      119 ValvalProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArg 158
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                                                                                                                                                                                                                                                                98
1 MetAsnTrpValTrpProLysThrLysSerWetSerPheLeuLeu---LeuIleThrPhe
                  25 TIGCATIGG-----ACTAAAGCCAIGGACTICTIAATIAGICICAIGACCTIT
                                                                                                                                               313 GCTGCTAATCCTGAAGAAGCTGCAGAATCTCTGATTCCACTTCTAAAAGAAGCAGAAAATCT
                                                               20 LeuLeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeu
                                                                                                                                                                                                                                                         79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerTyr
                                                                                                                                                                                                                                                                               AlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAsp
                                                                                                                               40 AsnHisArgLysIleLeuPro---AsnGlnGluLeuLeuThrSerTyrAlaValIlePhe
                                                                                                                                                                                             59 AspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                     GIGGIICCIGIGAGCCAGCCAACCCAACACCCGTIAAGCIIGGGGCAACIGCAGGIITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysEheThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLys
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Sequence 1489 BP; 437 A; 284 C; 324 G; 444 T; 0 U; 0 Other;

1489

Length:

6.68e-162

Alignment Scores: Pred. No.:

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ValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138
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                                                     Etzler ME,
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DB:
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                                                                                1152
                                                                                                                                      416
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                                                               377
                                                                                                                                                                                                            GluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLysPheAsn 456
                           357
                                                                                                                                                                                                                                                                                                                                                                            NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note="These bases represent nucleotides missing from
/note="These payen in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this sequence"
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/note= "These bases represent nucleotides missing from
the sequence given in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this sequence"
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/note= "These bases represent nucleotides missing from
                                                                          LeuAspProGluGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleVal
ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla
                                                                                                    CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal---GluLysAspLys
                                                                                                                                      LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly
                           --Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the sequence given in the specification. They are included to maintain the nucleotide numbering give the specification for this sequence"
                           GlnLysAsnLeuvalValThrSerAlaPheTyrTyrArgSerSerGluValGly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NBP46 root lectin'
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                              AGATTAATGTATTTTATT
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/*tag= a
/product=
700. .702
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                                                                                                                                                                                                                                                                                                                                                                                                          Lotus japonica
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, expression of NBP46 can be used to medulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAsp 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AspalaGlySerSerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGCTGGTAGCACTGGAAGCCAGAGTCCATGTCTACAATTTTGATCAGAACTTAGATCTC
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                                                                                                                                                                                                                                                                                            New polynucleotides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1489
318
67
73
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Matches:
Conservative:
Mismatches:
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1674.00
82.62%
68.24%
69.63%
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98WO-US016261
                                                      97US-00907226
                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                  Murphy JB;
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25 TTGCATTGG-
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Best Local Similarity:
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132 28

19 72 252

78

312

86

372

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NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen; nitrogen; ss.
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                                                                                      /product= "NBP46 root lectin"
                                                                     complement (1. .1380)
                                                             Location/Qualifiers
                                                                                                                                             98WO-US016261
                                                                                                                                                               97US-00907226
                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                    Murphy JB;
                                                                                                                                                                                                                     WPI; 1999-167136/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                              P-PSDB; AAW85685
                                          sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
Percent Similarity:
                                                                                                                                           05-AUG-1998;
                                                                                                                                                            06-AUG-1997;
                                                                                                       WO9907223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                           18-FEB-1999
                                                                                                                                                                                                  Etzler ME,
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AlaglyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr
                                   GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysPheThr
                                               LysThrValGlyVallleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer
                                                                                  219 ArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLys
                                                                                                                          AGGAACACAGCTAAAAATGCTCCAAAANNNCCTGAAGGAGAGAGATCATAAAAAAGAAG
                                                                                                                                                 LeuValleuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn
                                                                                                                                                           GAAGCATTTCGTGCANNNATTTTCAAGGTCGCTGGTGCTTCTGCTAATCCTTGCATTTTA
                                                                                                                                                                                   AspalaalaargValLysIlePheLysThrThrAspGlyalaAlaSerProCysLeuLeu
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|GCTGGCTTTGAYGGGCATATACATATTCCGGAGCAGAGTATAAGGTCTCGGCCCCAGCT
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                                                                                                                                                                                                                                                                       ProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyJserGly
                                                                                                                                                                                                                                                                                                            GlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe
                                                                                                                                                                                                                                                                                                                                               ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla
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|TGTAAAACAAATCTTGAGGATGCAAAATACCCAGATCTTTATGAGAAAGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleVal
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerArg
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Matches:
Conservative:
Mismatches:
Indels:
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Example 2; Page 49-51; 57pp; English.
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1654.50
82.75%
67.03%
68.82%
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à d ò

> entry) CDNA.

(first

19-JUL-1999

NBP46 (root lectin)

LNP

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corhizal infection, useful for improving plant growth, plant cell with a sequence encoding lectin/nucleotide
                                                                                                            DNA encoding Lotus japonicus lectin/nucleotide phosphohydrolase,
                                                                                                                            Lectin/nucleotide phosphobyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein; nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth;
                                                                                                                                                                                                                      *tag= a
product= "LNP"
/note= "Lectin/nucleotide phosphohydrolase"
                                                                                                                                                                                                                                                         /note= "No start or stop codon given"
/transl_except= (pos:1024. .1026, aa.Ala)
/transl_except= (pos:1478. .1380, aa.Xaa)
/transl_except= (pos:1435. .1410, aa.Xaa)
/transl_except= (pos:1435. .1437, aa.Xaa)
                                                                                                                                                             plant development; antisense technology; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulating mycorhizal infection, useful transforming plant cell with a sequence phosphohydrolase.
                                                                                                                                                                                                                                                                                                             "Xaa= Stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 32-34; 37pp; English.
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                 corniculatus var. japonicus.
                                          BP
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                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001; 2001WO-US028165
                                           DNA; 1458
                                                                                 (revised)
(first entry)
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                                           standard;
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                                                                                 29-AUG-2003
18-JUN-2002
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                                                                ABK11099;
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                                                                                      GluLysileLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln
                                                                                                                                                                  AsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeu
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                                    GluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro
                                                LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla
                                                                                                                                  GAAAAGATATTGCAAGCGACAAGGAATATGTTCAGCAACAGAAGTACCCTCAACGTTCAA
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The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNF (lectin/nucleotide phosphotydrolase) polynucleotide, or its complement. The LNF's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of mutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Lotus japonicus lettin/nucleotide phosphohydrloase (LNP) that can be used to modulate mycorrhizal infection in plants. (Updated on 29-AUG-2003) Other; BP; 438 A; 267 C; 309 G; 444 T; 0 U; 0

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Ecto-phosphatase; drug resistance; ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roux SJ,
                                                                                                                                                                                                                                                                                                                                                                                     Ecto-phosphatase coding sequence.
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                                                                                                                                                                                                                                                                                                                         DNA; 1661
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                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                        AAA96064 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TEXA ) UNIV TEXAS
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The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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GITIACCCT-----ACACAAIGGAGTICCTIAITAAACTIAICACTITICIACIATITI
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                                                                                 TITAATAAATGCAAAAACACAATTCGTAAGGCTCTTAAGTTGAACTATCCATGTCCATAT
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|2218 GTATGCATGGATCTTATATATCAGTATGTGTTACTCGTTGATGGATTTGGTCTTGATCCA
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/product= "blight resistance protein"
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                                                                                                                                                                  343 ValValThrSerAlapheTyrTyrArgSerSerGluValGlyPheVal-----ThrPro 360
                                                                                                                                                                                                                                                                                             ValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspPro
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                                                         GGAATCTATACATATTCAGGGAGAAGATTTAAGGCAACTGCTTACACTTCTGGTGCAAAC
                                                                                 PheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHis
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                 GCCGAGATTTTGAAGCTCACTCCTTCTCCTAACCCTTGCCTTTTAGCTGGATTTAAT
                                       283 AspileTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsn
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                                             The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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                                                                                                                                                                                                                                                                                actggtagtcgcattcatgtttaccattttaaccagaacttagaccttcttcatattggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
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                                                                                                                                                                                                                           VallrpProLysThrLysSerMetSerPheLeuLeu---LeuIleThrPheLeuLeuPhe
                                                                                                                                                                                                                                                                      SerLeuProLysLeuSerSerGinTyrValGlyAsnSerIleLeuLeuAsnHisArg
                                                                                                535 A; 308 C; 306 G; 548 T; 0 U; 0 Other;
                                                                                                                               1697
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7
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Matches:
Conservative:
Mismatches:
Indels:
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                            4; Page 12-13; 20pp; Japanese
                                                                                                                                                                                                          x AAF85680
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1570.50
80.78%
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65.33%
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Best Local Similarity:
                                                                                                     Sequence 1697
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                                                      270 AspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGly
                                                                    378 CCTCGTTCTCCTAACCCTTGCCTTTTAGCTGGATTTAATGGAATCTATACAGGG
                                                                                                                               838 AGAAGATTTAAGGCAACTGCTTACACTTCTGGTGCAAACTTTAATAAATGCAAAAACACA
                                                                                                                                                                      898 ATTCGTAAGGCTCTTAAGTTGAACTATCCATGTCCATGTCCATATCAGAATTGCACTTTTGGTGGA
                                                                                                                                                                                                                                                                                                                    ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr
                     310 AlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGly
                                                                                                                                                                                                     330 iletrpaspelyelyselyserelyelniysasnieuValValThrserAlaPheTyr
                                                                                                                                                                                                                                                     350 TyrargSerSerGluValGlyPheVal-----ThrProProAsnSerLysAsnArgPro
                                                                                                                                                                                                                                                                                                      368 LeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSer
                                                                                                                                                                                                                                                                                                                                                                        388 ThrPheProAsnValGluLysAspLysLeu---ProPheValCysValAspPheThrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1198 CAGTATGTGTTACTCGTTGATGGATTTGGTCTTTGATCCATTGCAAAAGATTACATCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/*tag= a
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61. .1401
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                                                                                              The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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TIGCAATCGGIAAGGGATAIGCTGAGCAACAGAAGTACCTICAACGTTCAACAGAGGGA
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|TIGGGAAAITTAGGGAAAAAGTACACAAAAACAGTIGGAGTAATAGAICTIGGAGGIGGA
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                                  New blight-resistant polypeptide useful for giving blight resistance
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                                                                                                                                                             Sequence 1368 BP; 422 A; 260 C; 275 G; 411 T; 0 U; 0 Other;
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298
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                        Claim 3; Page 12; 20pp; Japanese
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1569.50
81.36%
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WPI; 2001-320697/34.
P-PSDB; AAB81952.
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Query Match:
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1138 AAGGTTGCTTGTAGCACAGAATTAAAGGATCTCAAGTCCGTTTTCCCTCGTGTTAAGGAT 1197
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| AATGCAACATGCTCTTATAAGGATTGCACTTTCGGAGGCATATGGAATGGCGGTGGTGGTGGTGGT
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                                                                                                                                                                                                                   PheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerVallleAspGlyThr 176
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                                                                                                                                                                                                                                                                                                                             GlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAlaSerProCys
                                                                                                                                                                                                                                                                                                                                                                                                                             838 ATTITGTCTGGITTTGATGGGTATTACACATACGGAGGTCCAGTATAAAGCCACAGCT
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                                                                                                                                                           TATTCAAAGACGGTTGCTGTAGTTGACCTAGGTGGTGGATCTGTTCAAATGGCTTACGCA
                                                                                                                                                                                                                                                                                 ACCGAGATGTTCCTCAGGGGAAAGAATATTACCTCTATGTACACAGTTACTTGCGTTAT
                                                                                                                                                                                                                                                                                                                                                ValSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMet
                                                                                                                                                                                                                                                                LysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyr
                  ::: |||||||:::||| |||:::||| CTGAAGAAGAGAAGCACATTGAGTGCAAAC
                                                                GlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLys
                                                                                                                                PheThriysThrvalGlyvalIleAspLeuGlyGlyAlaSerValGlnWetAlaTyrAla
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                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell plantacteristic of a stress response. The method is useful in the plant cell production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliam stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                    Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                   ds.
              thaliana; plant; gene; stress; transgenic;
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Matches:
Conservative:
Mismatches:
Indels:
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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1281.50
74.15%
54.88%
53.31%
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                    24-AUG-2001; 2001WO-US026685
                                                                                                                                                                                                                                                                         Harper JF, Kreps J,
                                          Arabidopsis thaliana
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               Arabidopsis
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The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynuclectide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell genome, and for augmenting a plant genome, by contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell to produce a differentiated transformed plant. The sequences shown in ABZ421017 - ABZ42142 represent segments of A. thaliana cDNA modulated by PTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression
and for augmenting
                                                                                                        Posttranscriptional gene silencing, PTGS; plant; transformation; gene;
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Matches:
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1. .1419
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                                                       entry)
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Best Local Similarity:
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                                                     TyrGlnAspAlaileValGluThrAlaTrpProLeuGlyThrAlaileGluAlaileSer
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Whitham S, Xie Z,
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Katagiri
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US-09-657-631-2 (1-462) x ADA68447 (1-1419)

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150 91 ATTGTGTTGATCGGTCTCGTTCTTCTGCTAATGCCTGGGAGATCGATTTCTGATTCCGTC LeuLeuLeulleThrPheLeuLeuPheSerLeuProLysLeuSerSerSerGlnTyrVal 14

991 CTAAAAGTGAATGATGACACTGTGTACACATGAAATGCACATTCGGAGGAGGAGTCTGGAAT 1050 1170 GITGAAGAGTAITCIGIGCATAATCGCAAAGGAGGTCCTAAITCGAGAGGTCCGAAGAAT 210 113 450 153 510 173 193 630 810 213 069 233 750 253 273 lleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 313 352 GlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSer 53 73 93 390 391 AsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeu 410 TyrAlaValIlePheAspAlaGlySerSerGlySerArgValHisValPheAsp GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysPro 391 GACAAAGCTTCTGTTCCCCGTCACCTCCAAAGACACATGTCAGAGTTGGC ArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerVallle GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeu GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly AlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaVal AspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeu LeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAla 751 TCATATGTCAGAGAGGATGTATCTGAAGGGACGGAAGTATTTCCTCTATGTTCACAGTTAC AlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAsp 234 ProTyrMetLysLysLeuValLeuLysGlyLysLysLysTyrAspLeuTyrValHisSerTyr 274 SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn LeuArgLeuAsnGluPro---CysSerHisGluAsnCysThrPheGlyGlylleTrpAsp GlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgser SerGluValGlyPheValThrPro-----ProAsnSerLysAsnArgProLeuAspPhe GluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPhePro 1171 GAGAAAGCAGCAAAGAAAGCTTGTAGTATGAAGCTGGAAGAAGGGAAAATCAACGTTCCCA 151 74 94 331 114 54 154 294 174 214 691 871 254 811 333 371 353 q à g Dp ò à g ð g qq g à ð  $\delta$ d ð 셤 ò à g à qq ò Q  $\delta$ Dp à qq d g

Search completed: August 19, 2004, 15:27:50 Job time : 552.212 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 19, 2004, 14:05:21; Search time 3567.58 Seconds (without alignments) 3867.136 Million cell updates/sec
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2404
1 MNWVWPKTKSMSFLLLITFL.....GTAIEAISSLPKFNRLMYFI 462
OM protein - nucleic search, using frame_plus_p2n model
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Perfect score:
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0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Sequence:

55026578 Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST:\* Database :

gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_estfun:\*
em\_estfun:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_esthum:
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em gss\_pln:\*
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em gss\_fun:\*
em gss\_mam:\* em\_gss\_pro:\*
em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* ew das wns:\* 

## gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Ouerv				
No.	Score	Match	Length	DB		escription
1	943	6	74	13	BQ1651	0165194
7	9	φ.	745	12	448	4489
m		ω.	760	12	8443	84413
41	ĕ	'n.	651	12	6732	67324
ı,		34.7	673	13	4841	8414
9 1	54	4.	929	12	6573	65733
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σ,	ĕ	ά.	658	12	26310	63104
10	07	'n.	658	10	54162	41625
11		m	651	12	4901	49019
12	ÖŢ,	'n	629	10	54179	11795
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. 14	94.	Ε.	664	12	26500	55005
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16		ς.	808	14	13780	37805
17	83.	ď	655	12	5345	195
18		۲,	862	14	3460	34605
19		ď.	772	14	3574	35745
20	77	ď	652	12	703E	70380
21		~	726	13	5525	5293
22	77	ď	650	12	59/5	57694
23	767.5	$\vec{}$	622	10	3904	143
24	67.	_;	658	13	3696	36907
25	9	_;	648	12	5535	55356
26	76		663	12	5732	57321
27	61.		643	10	2234	22347
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29	59.	_:	735	13	5541	55419
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31	•	_:	680	10	1330	11307
3 2	75	ᆣ.	629	10	3916	39165
33	54.	:	620	12	5768	57682
34		31.4	624	10	243	12432
3.5	27	-:	883	12	1728	17286
36	75	:	732	14	47	00476 saul7a01
3.7	20	:	611	17	5770	57700 NF113G12
38	φ.	:	653	13	636	46365 NF047F08
39	42.	_:	625	12	I26458	54586 NF117C01
40	36.	ς.	992	14	337	3377 EST67972
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	73		1138	14	21041	0411 FGAS0222
44		_:	657	10	58459	84590 N210666
	m	_:	631		26575	265759 NF093F

## ALIGNMENTS

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Medicago truncatula (barrel medic)
Medicago truncatula
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/cultivar="genotype A17"
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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/note="Vector: pBluescript SK-; Site 1: BcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack II Gold packaging
Stratagene and packaged using Gigapack IIs were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 CAATATCTTGGAAACAACATATTACTCACTAACCGTAAGAATTTTCCCAAAACAAGAACCA
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                                                                  Town, C.D., Van Aken, S.
                                                                                                                                                                                                                  Department of Plant Biology
University of Minnesota
20 Blosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
210 Blosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
220 Blosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
220 Blosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
220 Blosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
220 Fixer: Standenb@cbs.um.edu
220 Fixer: Standenb@cbs.um.edu
230 Fixer: Standenbu.edu
230 Fixer: S
                        1 (bases 1 to 743)
Vandenbosch, K., Endre, G., Silverstein, K., Town, C.D., Van Ake Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and re-arrayed (2002)
Unpublished (2002)
Contact: VandenBosch K.
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Conservative:
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Indels:
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/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally lagated into the Unizap KR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 24-APR-2001
M24 5' end,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 719
                                                                                                           SerVall1eAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeu 190
                                                                                                                                                                                                                                210
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                                                                                                                                                                                                                                                                                                                                            211 ValGlinMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProProGln 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSer
                                                                                                                                                                                                                                                              600 GIICAAAIGGCAIAIGCAGIGICAAAGIAIACAGCIAAAAAIGCICCAAAAGIIGCIGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 GlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrVal
151 GlnAlavalArgGluMetPheArgAsnArgSerSerLeuServalGlnProAspAlaval
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VandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D.,
Bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula 72 h after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Biology
University of Minnesota
202 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
Tel: 612 624 2755
Pax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: kvandenb@cbs.umn.edu
M392896e TIGR sequence name: MTBBP84TK More information
M392806e TIGR sequence name:
available at: www.medicago.org
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. ~45s
/organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG644489 1inear EST
ESTS06108 KV3 Medicago truncatula cDNA clone pKV3-37M24
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Pred. No.:

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ORIGIN

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Utterback, T., Cho, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="roots colonized with Glomus versiforme"
/dev stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 CTCACTAAT --- CGAAAGATTTTCCAAAACAAGAAACAATTTCCTCTTATGCTGTCGTG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             mixed
                     Medicago truncatula/Glomus versiforme mixed EST library Medicago truncatula/Glomus versiforme mixed EST library Eukaryota; mixed EST libraries.

1 (bases 1.0 760)
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Chand Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thr Pheleu Leu Phe Ser Leu Pro Lys Leu Ser Ser Gln Tyr Val GlyAsn Ser Ile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 LeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIle
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                                                                                                                                                                                                    Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrisonGacoble.org
Noble EST name: N379883e TIGR sequence name: MTDBQ16TK More information is available at: http://www.medicago.org
Seq primer: SKmed (CTA gAA CTA gtg gAT CC).
Location/Qualifiers

    .760
/organism="Medicago truncatula/Glomus versiforme

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Medicago_truncatula_genotype_A17"
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179
36
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Matches:
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/clone="pMHAM-15D7"
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                                                                                                                                                                Glomus versiforme, 2001
Unpublished (2001)
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                                            ORGANISM
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                                                                                                         AUTHORS
                                                                                  REFERENCE
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      KEYWORDS
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                                                                                                                                             TITLE
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BG584413. GI:13599477
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TCAGCGCTCCAAGACACCCATTAGACTTGGGGCAACAGCAGGTTAAGGCTTTTGAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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LOCUS

BG584413 RESULT 3

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ACCESSION VERSION

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/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by spodoptera exigna (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 TTATCTCTGGGTGACAGTTAACTATGCATTGGGGAAATTGGGAAAAAATTCACAAAAAC
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                                                                                                                                                                                                                                                                   HisarglyslleLeuProAsnGlnGluLeuLeuThrSerTyralaValllePheAspAla
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Conservative:
Mismatches:
Indels:
Gaps:
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NF068A12FL1FL097 Developing flower
NF068A12FL 5', mRNA sequence.
BQ148414
                                                                                                                                                                                                                                         (1-651)
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                                                                                                                              1.04e-90
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89.77%
76.74%
35.77%
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Best Local Similarity:
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NF105B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone
NF105B12IN 5', mRNA sequence.
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Medicago truncatula
Subaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Pabales, Fabaceae, Papilionoideae, Trifolieae,
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                                        GAAGGTTCTTATCTCTGGGTGACAGTTAACTATGCATTGGGGAATTTAGGGAAAAGGTAC
                                                                                                   LeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPhe
                                                                                                                      158 ArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGln
                                                                                                                                                                                  GluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPhe
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           TATGCAAATGATCCGGAACAAGCTGCAAAATCTTTGATTCCACTTCTACAACAAGAAA
                                                                                                                                                                                                                                                                                            ThriysThrvalGlyValIleAspLeuGly-GlyAlaSerValGlnMetAlaTyrAlaVa
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                                        AspvalvalproGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGly
                                                                USA
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Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USF
Tel: S01 575 5191
Fax: 501 575 7601
Email: kkorth@comp.uark.edu
Insert Length: 651 Std Error: 0.00
Plate: 105 row: B column: 12
Seq primer: TCACACAGGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="NF105B12IN"
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/dev stage="mature"
/clone_lib="Insect herbivory"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Medicago truncatula"
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/db_xref="taxon:3880"
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mRNA linear EST 24-APR-2002 Medicago truncatula cDNA clone

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/dev stage="matter" //dev stag
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     GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp 142
                                                                                                                                143 GlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSer 162
                                                                                                                                                                                                                                               163 LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu 182
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Entaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots,
rosids; eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
Medicago.
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NF093B10IN1F1089 Insect herbivory Medicago truncatula cDNA clone
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
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Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, 171: 501 575 5191
Fax: 501 575 7601
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Conservative:
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Insert Length: 656 Std Error: 0.00
Plate: 093 row: B column: 10
Seg primer: TCACACAGGAAACAGCTATGAC.
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|db_xref="taxon:3880"
|clone="NF093B101N"
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/tissue_type="Developing flowers"
/fersue_type="Developing flowers"
/dev_stage="Developing, fully-opened flowers and flowers in early transition into pods."
/clone_tis="Developing, flower."
/clone_tis="Developing flower."
/clone_tis="Developing flower."
/clone_tis="Developing flower."
/note="Vector: Lambda Zap; cDNA was prepared from polyA+enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The CDNA was directionally ligated into the Uni-Zap Xx vector Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap Xx vector using ExAssist helper phage and the E. coli strain
Xill-Blue MRF. (Stratagene). Excised plasmids were plated
                                                                                   Bell, C.J.,
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                             Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J Frlores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                              Email: gdmay@noble.org
Insert Length: 673 Std Error: 0.00
Plate: 068 row: A column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                  Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OX
Tel: 580 221 7391
Fax: 580 221 7380
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/db_xref="taxon:3880"
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Best Local Similarity:
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NFOSSFILSTIF1000 Developing stem Medicago truncatula cDNA clone
NFOSSFILST 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 LeuServalGinproAspAlayalServalIleAspGlyThrGlnGluGlySerTyrLeu 182
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                GluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGlu 122
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Contact: Dixon RA
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GATCAGCGCTCCAAGACACCCATTAGACTTGGGGCAACAGCGGGTTTAAGGCTTTTGAAT
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                                                                                                                                                                                                                                         CTTIGGCAAAACCCAAGAATATGATGAACTTTATGACACTCATCACATTCTTCTTTT
                                                                                                                                                                          LysileLeuProAsnGlnGluLeuLeuThrSerTyrAlaValllePheAspAlaGlySer
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                                                                          VallrpProLysThrLysSer---MetSerPheLeuLeuleulleThrPheLeuLeuPhe
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Mismatches:
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Plant Biology Division
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | LeuSerValGlnProAspAlaValSerVall1eAspGlyThrGlnGluGlySerTyrLeu 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 AAAGAIGIIGAGIIIITAIAAIAAGACACGCCGGGIITIGAGIGCAIACGCGGGAIAAICCA
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                                                                                                                                                                                                                                                                             /dev_stage="Pooled developmental"
/dlone_lib=lpeveloping stem"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
                                                                                      MGI:S:16915
                   USA
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157
24
1
                   73402,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 7340 Tel: 580 221 7302 Fax: 580 221 7380 Email: radixon@noble.org Medicago Genome Initiative accession: MG Insert Length: 660 Std Brror: 0.00 Plate: 0.55 row: F column: 11 Seq primer: TCAGACAGGARACAGCTATGAC.
                                                                                                                                                                          1. .660
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/mol_type="mRNA"
/db_xref="taxon:380"
/clone="NPO55F115T"
/tissue_type="stem"
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824.50
88.43%
72.69%
34.30%
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Lu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J. Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Contact: Harrison M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7326 Eax: 580 221 7386 Std Error: 0.00 Flate: 038 row: F column: 11 Flosert Length: 658 Std Error: 0.00 Flate: 038 row: F column: 11 Seq primer: TCACACAGGANACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       658 bp mRNA linear EST 18-JUL-2001
clone NF038F11FL 5', mRNA sequence.
                                   SerProCysLeuleuAlaglyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293
                                                       427 GCATCCGCTCCACCTTCCGGTGCTAGTTACTCAAAATGCAAGGATGATGCAGTGAAAGCC 486
                                                                                                                                                                                                                                                                                               294 IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 313
                                                                                                                                                                                                                                                                                                                                                   354 GluValGlyPheVal-----ThrProProAsnSerLysAsnArgProLeuAspPheGlu 371
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                          314 LeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGly
                                                                                                                                                                                                                     334 GlyLysGlySerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSer
                                                                                                                                                                                                                                                                                                                                                                                       607 GAGGCTGGATTTGTTAACGCCCAATGCGCCTGTCGCTAAGGTTAAACCATCGGACTTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 ThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsn
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/dev_stage="trifoliate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliate stage,
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/db_xref="taxon:3880"
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clade, Panicoldeae, Andropogoneae, Zea.
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/culfivat="W22"
/culfivat="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm 5"
/note="Vector: pBluesGript SK-; Site_1: BcoRI; Site_2: %Note="Vector: pBluesGript SK-;
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Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E.
Messing,J.
                                                                                                       il bp mRNA linear EST
Zea mays cDNA, mRNA sequence
                               629
Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsheng
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Freinghuysen Rd., Piscataway, NJ 08854, USP
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
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 truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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S Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

L Contago truncatula insect herbivory library

London Flore (2000)

London Factor of Nathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 5191

Fax: 501 575 7601

Email: kkorth@comp.uark.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /mol_type="mrna" | /db xref="taxon:3880" | /clone="nro65A041N" | /tissue type="local and systemic leaves" | /clone lib="mrsect herbivory" | /clone lib="nrosct herbivory" | /clone lib="nrosct lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by expanded M. truncatula leaves of plants fed upon by expanded leaves from injured plants) and wounded leaves were harvested and pooled."
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                     0.00
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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

FEATURES

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NF067E07IN1F1054 Insect herbivory Medicago truncatula cDNA clone
NF067E07IN 5', mRNA sequence.
                                                                     83 AsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysPro 102
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
                                             23 SerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArg
                                                                                                                                                                                          SerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGly
                                                                                                                                                                                                               123 GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                  379 GATCAGCGCTCCAAGACACCCATTAGACTTGGGGCAACAGCAGCTTTAAGGCTTTTGAAT
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                                                                                                                    Lys11eLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySer
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217 Plant Science Building, Fayetteville, AR
1815 501 575 5191
Fax: 501 575 7601
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Insert Length: 659 Std Error: 0.00
Plate: 067 row: E column: 07
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers
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Medicago truncatula
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Dept. of Plant Pathology
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/clone_lib="Insect herbivory"
/clone_lob="Insect herbivory"
/clone_vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
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                                                                                                                                                                                                                                                                                                                                    cDNA clone
                                                                           TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
                                                                                                                                                          163 LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu
                                                                                                                                                                                                                                                                                                     NP003H05INIF1048 Insect herbivory Medicago truncatula NP003H5IN 5', mRNA sequence.
                                                                                                                                                                                                203 ValileAspLeuGly-GlyAlaSerValGlnMetAlaTyrAlaVal 217
                                                                                                                                                                                                                      tissue_type="local and systemic leaves"
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Matches:
Conservative:
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Indels:
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clone="NF003H05IN"
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Insert Length: 651 Std Er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="mRNA"
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BG449019.1 GI:13367800
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88.15%
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Best Local Similarity:
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Query Match:

Pred. No.:

Score:

ORIGIN

438 162

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Location/Qualifiers
1. .665
NF098A09IN 5', mRNA sequence.
                                                                                                                                                                                                                            Contact: Korth K
Dept. of Plant Pathology
                         GI:14871547
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800.50
86.92%
71.03%
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NF098A09INIF1069 Insect herbivory Medicago truncatula cDNA clone
                                                                     /tissue type="local and systemic leaves"
/dev stage="mature"
/clone lib="Insect herbivory"
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155
34
26
1
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Conservative:
Mismatches:
Indels:
              /organism="Medicago truncatula"
/mol type="mRNA"
/db_xref="taxon:3880"
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                                                              clone="NF067E07IN"
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71.43%
33.34%
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DEFINITION
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/clone="NF098A09IN"
/tissue type="local and systemic leaves"
/tissue type="local and systemic leaves"
/dov_stage="mature"
/clone lib="locat herbivory"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (bet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysPro 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGAIGTIGAGIIIITAIAAIAAAGACAACGCCCGGIIITGAGIGCAIACGCGGAIAAICCA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                    Tracheophyta;
                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                 Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Stpressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 CTTTGGCAAAACGCAAGAATATGATGAACTTTATGACACTCATCACATTCTTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysileLeuProAsnGlnGluLeuLeuThrSerTyrAlaValilePheAspAlaGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ValTrpProLysThrLysSer---MetSerPheLeuLeuLeuIleThrPheLeuLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArg
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                                                 Embryophyta;
                                                                                                                                                                                                                                                                                                                                                        University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701,
7217 Plant Science Building, Fayetteville, AR 72701,
Fax: 501 575 7601
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152
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Matches:
Conservative:
Mismatches:
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                            Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kkorth@comp.uark.edu
Insert Length: 665 Std Error: 0.00
Plate: 098 row: A column: 09
Seg primer: TCACACAGGAAACAGCTATGAC.
Medicago truncatula (barrel medic
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BI272922 625 bp mRNA linear BST 18-JUL-2001
NF091F05FL1F1046 Developing flower Medicago truncatula cDNA clone
NF091F05FL 5', mRNA sequence.
                                                                                                                                                                                                                                                 71 AATATACTCACCAAT---CGTAAAATATTTCCAAAACAAGAAACTCTAACCTCGTACGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                               SerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 AGTGCATACGCAGATAATCCAAAGGAAGCAGCAGAGTCTCGTGATTCCACTTTTAGAGCAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AlagluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThr 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 AlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 LysPheThrLysThrValGlyVallleAspLeuGlyGlyAlaSerValGlnMetAlaTyr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 GALTITICAGAGACAGTGGCAGTAGCTGATCTTGGAGGGGGATCAGTTCAAAATGGTATAT 607
                                                                                                                                                         11 CICATCACATTICTACTCTTCTTGATGCCTACAATCTCTTCCTCCCCAATATCTTGGAAAC
                                                                                                                                LeulleThrPheLeuLeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsn
                                                                                                                                                                                                            SerIleLeuLeuksnHiskrgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAla
                                                                                                                                                                                                                                                                                        ValllePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsn
                                                                                                                                                                                                                                                                                                                    128 GICGICITIGAIGCIGGTAGCACCGGTAGCCGIGTICAIGICTACCATTITGAICAGAAC
                                                                                                                                                                                                                                                                                                                                                                   LeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 ThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AlaValSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspPro 234
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The Samuel Roberts Noble Foundation
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                                                       Gaps:
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            Similarity:
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                              Query Match:
DB:
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B1265005

664 bp mRNA linear EST 18-JUL-2001
NF004G10IN1F1084 Insect herbivory Medicago truncatula cDNA clone
                                                                   142
143 GlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSer 162
                                                                                                                                                           163 LeuSerValGinProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu 182
                                                                                                                                                                                                                                                                   560
                                                                                                                                                                                                                                                                                                        202
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
                                                           GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp
                                                                                                                                                                                                                                                                                                183 TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
                                                                                                                                                                                                                                                                                                                                   sei regereachtaachareartregeaaarregeaaaarteacaaaaaacaeaa
                                                                                                                                                                                                                                           University of Arkansas 1
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: S01 575 5191
Fax: S01 575 7601
                                                                                                                                                                                                                                                                                                                                                                         203 VallleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAla 216
                                                                                                                                                                                                                                                                                                                                                                                                              621 GTAATGGATCTTGGANGTGGATCANNTCAAATGGNNTATGCA 662
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155
28
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kkorth@comp.uark.edu
Insert Length: 664 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 004 row: G column: 10
Seg primer: TCACACAGGAAACAGCTATGAC.
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Medicago truncatula
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'db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NF004G10IN 5', mRNA sequence
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BI265005.1 GI:14867791
EST.
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83.56%
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Percent Similarity:
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BI265005
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KEYWORDS
SOURCE
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195

664

ORIGIN

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Search completed: August 19, 2004, 20:31:51
Job time : 3575.58 secs
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/dev_stage="Developmentally pooled. Contains a mixture of
/dev_stage="Developmentally pooled. Contains and flowers
in early transition into pods."
/clone lib="Developing flower"
/clone lib="Developing flower"
/note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The CDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
in vivo excised from the recombinate Uni-Zap XR vector
using ExAssist helper phage and the E. coli strain
XIII-Blue MRRF' (Stratagene). Excised plasmids were plated
using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLys 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 ValvalprogluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAGAAGTACCTTCAATGTTCAACCTGATGCAGTTTCTATTATTGATGGAACCCAAGAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGlu
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Fax: 580 221 7380
Email: gdmay@noble.org
Insatt Length: 625 Std Brror: 0.00
Plate: 091 row: F column: 05
Seg primer: TCACACAGGAAACGCTATGAC.
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF091F05FL"
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Best Local Similarity:
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APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-07981008
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
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VHER INFORMATION: NBP46 (DB46) No. 6465716 factor binding lectin NAME/KEY: mat.peptide
LOCATION: (195)..(1436)
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Mismatches:
Indels:
Gaps:
US-09-557-800C-52
US-09-608-28A-26
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Matches:
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PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
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Patent No. 6465716
GENERAL INFORMATION:
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SEQ ID NO 1
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Best Local Similarity:
NAME/KEY: CDS
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   August 19, 2004, 14:16:56; Search time 94.8078 Seconds (without alignments) 2704.285 Million cell updates/sec
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3, Appli
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                                                                                                                                                                                                1 MNWVWPKTKSMSFLLLITFL......GTAIEAISSLPKFNRLMYFI 462
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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_6/ptodata/2/ina/backfiles1.seq:*
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US-09-129-112-3
US-09-129-112-13
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US-09-608-285A-48
US-09-608-285A-26
US-09-608-285A-52
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US-09-570-608-285A-52
US-09-570-539-1
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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2404
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APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-07981005
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
  380
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    ProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeu
                                                   ThrpheGluGluAlaLysSerThrPheProAsnValGluLysAspLysLeuProPheVal
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; Sequence 3, Application US/09129112
; Patent No. 6465716
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ORGANISM: Dolichos biflorus
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184 GICCATGITTACCATTTTGATCAGAACTTAGATCTACTTCACATTGGCAATGATATTGAG
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                    LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly
                                                                            nAspAlalleVal
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APPLICANT: Etzler, Judith B.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume F
TILE REFERENCE: 023070-079810US
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US 08/907,226
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR APPLICATION DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN OF 2.1
                                                                             LeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyrGl
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Mismatches:
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LOCATION: (1)...(1458)

COTHER INFORMATION: full length cl.
NAME/KEY: CDS

LOCATION: (13)...(1380)

CTHER INFORMATION: NBP46

NAME/KEY: modified base

LOCATION: (1)...(1458)

COTHER INFORMATION: n = g, a, c or US-09-129-112-8
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67.03%
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58 ACTGCAACTGCAAGTTCCTTTTCCCTCCATGGGAAGGGCTTCAAGCATCGCAAG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 PheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThr 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLys 196
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                                                                                                                                                                                                                                                                                                                                                            10 SerMetSerPheleu---LeuleulleThrPheleuleuPheSerLeuProLysLeuSer
                                                                                                                                                                                                                                                                                                                                                                                  4 AGCATGATTTCTCATAATCCTATTTTCTCTTCTCTGGACGCTG-----GTTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 TATICAAAGACGGTIGCIGIAGIIGACCIAGGIGGIGGIGGAICIGIICAAAIGGCIIACGCA
                                                                                                                                                                                                     1434
255
90
106
17
                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                  29 SerSerGlnTyrValGlyAsnSerIleLeuLeuAsn-
                                                                                                                                                                                                                                                                                                                           US-09-657-631-2 (1-462) x US-09-129-112-18 (1-1434)
                                                                                                                                                                                                     Length:
Matches:
                         primer
                                                                                        NAME/KEY: primer_bind
LOCATION: (1414). (1434)
COTHER INFORMATION: DEXBOLTOM primer
US-09-129-112-18
LOCATION: (1133)..(1151)
OTHER INFORMATION: DBX9-for/rev
NAME/KBY: primer bind
LOCATION: (1227)..(1247)
OTHER INFORMATION: DBX12 primer
                                                                                                                                                                                               4.62e-156
1341.50
73.72%
54.49%
55.80%
                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                  Alignment Scores:
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                                                                                                              Generace 18, Application US/09129112

GENERAL INCORATION:
GENERAL INFORMATION:
APPLICANT: ELzler, Marilynn E.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: AN O. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
FILE REFERENCE: 1998-08-04
PRIOR PILING DATE: 1998-08-04
PRIOR PILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 1434
            LOCATION: (1)...(1404)
OTHER INFORMATION: DBX gene involved in oligosaccharide signaling
NAME/KEY: sig_peptide
LOCATION: (1)...(60)
NAME/KEY: mat_peptide
LOCATION: (61)...(1404)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: DBX7-for/rev primer NAME/KEY: primer bind LOCATION: (667). (685)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: DBX1-for/rev primer NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: [688]. (704)
OTHER INFORMATION: DBX2-for/rev primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: Complement((1075)..(1093))
OTHER INFORMATION: DEX11 primer
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: Complement ((766)..(785))
OTHER INFORMATION: DBX10 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: Complement ((1)..(22))
OTHER INFORMATION: DEXLOP primer
NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (856)..(857)
OTHER INFORMATION: splice site
NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1071)..(1072)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (274)...(291)
OTHER INFORMATION: DBX8 primer
NAME/KEY: primer_bind
LOCATION: (297)...(314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: primer bind
LOCATION: (878)...(896)
OTHER INFORMATION: DBX5 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (955). (972)
OTHER INFORMATION: DBX4 primer
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OTHER INFORMATION: DBX6 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: DBX3 primer NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Dolichos biflorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (61)..(1404)
NAME/KEY: primer_bind
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LOCATION: (933)...(952)
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26

57 43 237

96

116

156

657 236 717 256 777

297

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GluaspileTyrargTyrSerGlyGluSerTyrasnileTyrGlyProThrSerGlyAla 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValSerValileAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 LeuglyLysLeuglyLysLysPheThrLysThrValGlyValIleAspLeuglyGlyAla 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 ValHisserTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AlaAlaSerProCysLeuLeuAlaGlyTyr 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GAAACCTTCAAA 486
                                                                                                                                                                                                                                                                                                                                                                                              TyralaVal11ePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 LysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeu
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|GGGAACTACTGGATGTTGCTAAACAGGACATTCCGTTGGAACTTCTGGAAGGCCACCCT
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136
70
151
60
13
                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                         US-09-657-631-2 (1-462) x US-09-608-285A-48 (1-2693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :::
CGGCCCCCAGAGAACTCCCACGTTAACCCAC
                                                                                                                                                                                                                                                                                     Indels:
Gaps:
                    09/118,205
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/116
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48
                                                                                                                                                                                                                 6.16e-52
506.00
49.40%
32.61%
21.05%
                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                               US-09-608-285A-48
                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                           LENGTH: 2693
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                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                     AATGCAACATGCTCTTATAAGGATTGCACTTTCGGAGGCATATGGAATGGCGGTGGTGGA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                            PheValThrPro----ProAsnSerLysAsnArgProLeuAspPheGluThrAlaAla 374
                                                                                                                                                                                                                                                                                                                                                                                                                 LysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLys 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGly 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheGlyLeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyrGlnAspAla 434
                                                       LeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGly 296
                                                                                                                                                                                                    AsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGly 336
                                                                                                                                                         837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 IleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLys
     ProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu
                                                                                                                                                                                                                                                                          SerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly
                                                                                            ATTITIGICIGGITITIGATGGGTATTACACATACGGAGGAGTGCAGTATAAAGCCACAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ford, Julio
APPLICANT: Yeung, George
JULIANG GEORGE
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR APPLICATION NUMBER: 09/244,444
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TTTGAGAAATTAATGTATTTCCTT 1401
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GENERAL INFORMATION:
APPLICANT: Ford, John
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US-09-608-285A-48
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Best Local Similarity: 32.61% Mismatches: 151 Query Match: 21.05% Indels: 60 DB: 4 Gaps: 13	(1-2693)			4	Oy 19s1leLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeu 109		547	130 LeulysLeuGlyhlaThrhlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIle				Db 724 GTITCCATCATGAACAGAACAGATGAAGGCGTTTCGGCGTGGATCACCATCACTTCCTG 783	Qy 190 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyAla 209	Db 784 ACAGGCAGCTTGAAAACTCCAGGAGGAGGAGCAGCGTGGGCGTGCTGGGCGGAGGA 843	Qy 210 ServalGlmMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 229	230 GlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyr 2	106	Cy 250 ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr 269   1		1009	282 GluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAla 301	1069	Qy 302 AsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316	1125 MGCLGCACAGGCIGGIGCIGCCAGAGGIGTCAGAGGCTCCTTCAAAACAGAGTGCACAGG 11	-	356	Db 1207GTGGACTTCTATGCTTTCTCCTACTATTACGACCTTGCAGCTGTGGGC 1257	Oy 357 PheValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLys 375
Oy 302 AsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316 :::::    ::: :::	317	1 7	1		1258 CTCATAGAIGCGGAGAAGGGAGCCAGCCIGGIGGGGGGAGTCGCAGTCGCA	Qy 376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp 395  Db 1318 TACGTGTTCGGACCTGGAGACACAGCCGCGAGAGCAGC  13.1 13.1 TACGTGTTCGGACCCTGGAGACACAGCCGCAGAGCAGC	396 LysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPhe	14	1408	452	Db 1456 GTTGAGACCAGCTCTGGGGGCCATTTTTCATTACATCGACTCCTC 1506	RESULT 7 US-09-557-800C-48	; Sequence 48, Application US/09557800C ; Patent No. 6476211	; GENEKAL INFORMATION: ; APPLICANT: Ford, John	<pre>// APPLICANT: Mulero, Julio // APPLICANT: Yeung, George // TITLE OF INVENTION: Methods and Materials Relating to CD39-Like // TITLE OF INVENTION: Not Consideration of the Constitution of the Constituti</pre>	FILE REFERENCE: 28110/36457; CURRENT APPLICATION NUMBER: US/09/557,800C	; CORRENT FILING DATE: 2000-04-25 ; FRIOR APPLICATION NUMBER: 09/481,238 : PRIOR FILING DATE: 2000-01-11		FILING DATE: 1999-0. APPLICATION NUMBER:	FRIOR FILING DATE: 1999-07-09 FRIOR APPLICATION NUMBER: 09/273447 DEFINE ETITING NAMES: 09/273447		APPLICATION N	; PRIOR APPLICATION NUMBER: 09/118,205 ; PRIOR FILING DATE: 1998-07-16	; NUMBER OF SEQ ID NOS: 56 ; SOFTWARE: Patentin Ver. 2.0	; SEQ ID NO 48 ; LENGTH: 2633	)	nment Scores:	Pred. No.: 6.16e-52 Length: 2693 Score: 506.00 Matches: 136 Percent Similarity. 40.4%

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1198 AGCCTGCACGAGCTGTGTGCTGCCAGAGTGTCAGAGGTCCTTCAAAACAGAGTGCACAGG 1257
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GERMEAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Wulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION NUMBER: US/09/608,285A
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR PILING DATE: 2000-06-25
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
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PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-07-06
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US-09-608-285A-26
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Best Local Similarity:
Query Match:
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           GlyLeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIle 435
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                                                                                                                       GTTGAGACCAGCTGGGGGCCCATTTTTTACATCGACTCCCTG 1575
                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION. METHODS AND MATERIALS RELATING TO CD39-LIKE TITLE OF INVENTION: POLYPEPTIDES TITLE REFERENCE: 28110/36570

CURRENT APPLICATION NUMBER: 2000-06-30
PRICE APPLICATION NUMBER: 09/583,231
                                                                                  ValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-04-25
PRIOR PLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR PLICATION NUMBER: 09/370,265
PRIOR PLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-07-09
PRIOR PLICATION NUMBER: 09/350,836
PRIOR PLICATION NUMBER: 09/350,836
PRIOR PLICATION NUMBER: 09/273,447
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-02-03-19
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1998-02-24
PRIOR PLING DATE: 1998-02-24
PRIOR PLING DATE: 1998-07-24
PRIOR PLING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                              Sequence 52, Application US/09608285A Patent No. 6335013
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506.00
49.40%
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21.05%
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APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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PRIOR FILING DATE: 2000-0
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US-09-608-285A-52
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Ford, J
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US-09-608-285A-52
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SEQ ID NO 52
LENGTH: 2762
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Pred. No.:
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                                                                                                                           1018 TCCTACAGCTACCTCGGGCTCGGGCTGATGTCGGCACGCCTGGCGATCCTGGGCGGCGTG 1077
                                                                376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp 395
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APPLICANT: FORG. John
APPLICANT: MISERO, JOHN
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILLE REFERENCE: 28111/35908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-07-09
EARLIER PILING DATE: 1999-07-09
EARLIER PILING DATE: 1999-07-09
EARLIER PILING DATE: 1999-07-09
EARLIER PILING DATE: 1999-02-04
EARLIER PILING DATE: 1999-02-04
EARLIER FILING DATE: 1999-02-04
EARLIER FILING DATE: 1999-02-04
EARLIER PILING DATE: 1999-02-04
EARLIER PILING DATE: 1999-02-04
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                                                                                                 282 GluAspileTyrArgTyrSerGlyGluSerTyrAsnileTyrGlyProThrSerGlyAla
                                                                                                                                                                                                                                                                                                                                                                      357 PheValThrProProAsnSerLysAsnArgProLeu---AspPheGluThrAlaAlaLys
                                  -AlaAlaSerProCysLeuLeuAlaGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 ValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeu 452
                                                                                                                                                                     AsnPheAsnGlu---CysArgAspLeuAlaLeuGlnIleLeuArg-----
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EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
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Patent No. 6447771
                                                                                                                                                                                                                                                                        1258 ACGCAGGAAGTGAAGCAT-
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                                       270 AspGly
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LENGTH: 2762
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                                                         APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
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Mismatches:
Indels:
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Matches:
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      Sequence 1, Application US/09240639
Patent No. 6350447
GENERAL INFORMATION:
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49.40%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                   -----CCTTCTCATGCATGGACCTCACCTAC---GTCAGCCTGCTACTCCAGGAGTTC 1476
                                                                                              357 PheValThrProProAsnSerLysAsnArgProLeu---AspPheGluThrAlaAlaLys 375
                                                                                                                                                                  376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp 395
                        337 SerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly 356
                                                                                                                                                                                                                                        396 LysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPhe
                                                                                                                                                                                                                                                                                                             416 GlyLeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26 Application US/09557800C

Sequence 26 Application US/09557800C

Patent No. 6476211

GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Perd, John
APPLICANT: Perd, John
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
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FILE OF INVENTION: MOTORER: US/09/557,800C
CURRENT APPLICATION NUMBER: US/09/557,800C

PRIOR PLING DATE: 2000-01-11
PRIOR FILING DATE: 1999-01-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PRIOR APPLICATION NUMBER: 09/224444
PRIOR APPLICATION NUMBER: 09/224444
PRIOR APPLICATION NUMBER: 09/224444
PRIOR PRILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-05
PRIOR PRILING DATE: 1998-07-24
PRIOR PRILING DATE: 1999-07-06
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LENGTH: 2762
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ORGANISM: Homo sapiens
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APPLICANT: Ford, John
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods with the CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR FILING DATE: 1999-00-01-11
PRIOR FILING DATE: 1999-00-01-11
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-09
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; ABPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD35
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-00-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-16
; PRIOR PRILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
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Best Local Similarity:
FILING DATE:
                                                                                                                                                                                US-09-608-285A-54
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                                                                                                                            357 PheValThrProProAsnSerLysAsnArgProLeu---AspPheGluThrAlaAlaLys 375
                                                                                                                                                                                                          AsnPheAsnGlu---CysArgAspLeuAlaLeuGlnIleLeuArg------Leu 316
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                                           250 ValHisserTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr
                                                                                                 ---AlaAlaSerProCysLeuLeuAlaGlyTyr
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APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1387 TACGTGTGTGTCGGACCCTGGAGACACAGGCGCAGAGCAGC-----
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CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
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PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/1618
PRIOR PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
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3ER: 09/583,231
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                                                                                                       270 AspGly---
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValSerVallleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeu 189
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1998-07-24
PRIOR PRILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VEY: 2.0
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282	302	316	336	345	357	373	393	413	433
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Search completed: August 19, 2004, 20:35:22 Job time : 114.808 secs

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Sequence 1, Application US/09129112
Batent No. US2002001995A1
GENERAL INFORMATION:
BAPLICANT: Etaler, Marilynn E.
APPLICANT: Etaler, Marilynn E.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
RIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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Sequence 3, Appli
Sequence 13, Appli
Sequence 8, Appli
Sequence 2234, Ap
Sequence 11084, Ap
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Sequence 1815, Appl.
Sequence 1888, Ap.
Sequence 1808, Ap.
Sequence 1908, Appl.
Sequence 2968, Appl.
Sequence 2403, Appl.
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Sequence 101749, Sequence 1923, Appl.
Sequence 24023, Appl.
Sequence 285, Appl.
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Sequence 285, Appl.
Sequence 287, Appl.
Sequence 288, Appl.
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Sequence 288, Appl.
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Sequence 48, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 52, Appl
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LOCATION: (51)..(1439)
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3654.341 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database

Description

Query Score Match Length DB

Sequence

Sequence Sequence Sequence

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of California
Factor Binding Protein From Legume Roots
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                                                                                                                                                                                                                                                                                                                                            CysvalAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGlu 420
TATGAAGATATATACAGATATTCCGGAGAATCGTACAATATCTATGGTCCCACTTCTGGT 950
                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAGATTACAGTGGCAGAAGAATTGAATATCAAGATGCCATTGTGGAAACAGCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                       GlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTrp
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Fatent No. US2020019995A1
GENERAL INFORMATION:
APPLICANT: Etaler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: THE REGENTS of the University of
TILE REFERENCE: 02070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
SOFTWARE PALENT NUMBER: US
SOFTWARE PALENT NOS: 19
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ORGANISM: Dolichos biflorus
FEATURE:
OTHER INFORMATION: genomic
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US-09-129-112-3
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; OTHER INFORMATION: NBP46 (DB46) No. US20020019995A1 factor binding lectin NAME/KEY: mat peptide ; LOCATION: (195)..(1436) US-09-129-112-1
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ζ	152	152
QQ	1635	CATITICCTIATGITATAACTACGCITICAAIGICTTAACTITICGITITICTCTCAIGTIG
ර් ස්	153	ValArgGluMetPheArgAsnArgSerSerVerUGlnProAspAlaValSer 171
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δ	184	1 1 1 1 1 1
qq	1814	TTTATCAGAATTCATTCTAATTTTTTTACTTAAGAAGATGGAAG
δλ	184	184
qq	1874	ACCTAGGACATTCATCTTATTAAAATAATTTATTGCAAAATAATACTATTTTTTAATTA 1933
٥y	184	184
QQ	1934	GAATTGATATTTGCGTATATTGTGAAAAGAAAGTAGATTGATT
٥x	184	184
ηρ	1994	GTATTTTAATAAATTTTTATTAACTCTTTTAACTTTTAAAAAA
δ	184	184
οp	2054	GTGTGTGGTGACATGCCCATACCCCATATGGACAATTACTGACATGCCATACCCGATATAT 2113
λõ	184	184
Dβ	2114	TAATATITITATCAATTGTCAATTTATTTATTGTAACTACTTTAAAAAATACTTTTAATTA 2173
δ	184	184
DÞ	2174	AATCATTGAGGTATCGCTTTAGTTTTTTTTTAAATTCGAAAAAATAATTAAT
λõ	184	184
Db	2234	GATATACTGGAAGAATTTCCGAAGGATATTCATATCCATATATAT
Qy	184	184
qu	2294	TITITATIGAACAAAIGCAACACIAICICIAAAIAIGAITITITITITIAIGIGGAAIGA 2353
δλ	184	184
QQ	2354	ATCACGACGATATAATTTTGTATAAGTAATTAAATTCACTATTCATTTTTATTTGTTGTG 2413
۵,	184	184
QQ	2414	TTTCTTTTAGGGTCCGCCAATTAGCTAAATCTTACCTAAAAAGATTGCAAACAAGAAA 2473
δλ	184	184
QQ	2474	AAGAAAGAAAGCAATGATGAAATTAAAAGTGGATCAAACCATGAGGATATGTTTCAAAAAG 2533
δ	184	184
Db	2534	AAGAATTAGGITCTTTGTTATGTTTTCAAAAACTAGTAGTTGGAATTTCTTAAATTCAAT 2593
δλ	184	184
qa	2594	TATAATTATTTAATAAAATTGTCTGCTTAATTGATAATATAAAAATAGCATAACTGATACA 2653
à	184	184

Percent Similarity: 83.05% Conservative: 68 Best Local Similarity: 68.45% Mismatches: 71 Query Match: 8 DB: 5	US-09-657-631-2 (1-462) x US-09-129-112-13 (1-1489)	Qy 1 MetAsnTrpValTrpProLysThrLysSerMetSerPheLeuLeuLeuIleThrPhe 19 :::::	20 LeuLeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeu 39	Db 73 GTGTTCATGTTAATGCCTGCTATCTTCTCCCCAATATCTCGGAAACAACATTCTCATG 132 Oy 40 AsnHisArdIvg1leLeuProAsnGlnGlnLeuTeuTertvalaValtleDha 58	133 AATCGTAAGATATTACTCCCCAAAAATCAGGAACCAGTTACATCATACGCTGTTATATTT	<pre>Qy 59 AspAlaGlySerSerGlySerArgValHisValPheAspPheAspGlnAsnLeuAspLeu 78                                      </pre>	Db 253 CTTCCCGTTGAAACGAACTTGAGTTTTATGATTCGGTTAAACCCGGTTTGAGTTCATAC 312 Ov 99 Alaarnivsbrochnivsalaalachnserientlebrolentenchnangholman 110	313 GCTGCTAATCCTGAAGAAGCTGCAGAATCTCTGATTCCACTTCTAAAAGAAGCAGAAAAT 37	Oy 119 ValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138	139 ArgLeuLeuAspGlyAspAlaAlaGluLySIleLeuGlnAlaValArgGluMetPheArg 15	Db 433 AGGCTTTTGGAGGGAATGCTGCTGAAAATATATTGCAAGGGGTCAGGGATATGCTCAGC 492 OV 159 ASRARGSPYSPYSPYAAJGJDPYABGRAJaVaJGGAVAAJTJGAARACJARTAGAA	493 AACAGAAGTGCCCTTAATGTTCAATCAGATGCAGTATCTATTCTTGATGGAACCCCAAGAA 55	Oy 179 GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThr 198	QY         199         LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer         218           Db         613         AAGACAGTGGGAGTAGTTGATCTAGGAGGTGGGTCAGTGCAAATGACATATGCAGTCTCA         672	23	QY       239 LeuValleuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn       258         Db       733 CTTGTACTCCAGGGAAAGAAATATGACCTTTATGTTCACAGTTACTTGCGCTATGGAAGA       792	0 0	279	Db 853 GCTGGCTTTGATGGGGGCATATACATATTCCGGAGCAGAGAGAG	Qy 299 SerGlyalaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGlu 318	33
Qy 343 ValValThrSerAlaPheTyrTyrArgSerSerGlu354 	Qy 354 354	Db 4934 GTTTACTTTGATTACTTATTTGTTTTATACCAATAAATTTTACATTATAGTTTATACTG 4993  Qy 355	GGTTGGTTTTGTCACTCCTCCAATTCCAAAATGGCCCT 5	5054 C		408 TyrThrLeuLeuValAspGlyPhe	LC.	GlyLeuAspProGluGlnGlulleThrValAlaGluGlylleGluTyrGlnAsp	5294 IIGGCAGGACTICCAGAGCAGAGATTACAGTGGCAGAAGGAATTGAATAT 434 AlalleValGluThralaTrpProLeuGlyThrAlalleGluAlalleSerSer	Db 5354 GCCATTGTGGAAACAGCATGGCTCTAGGAACTGCCATAGAAGCCATATCATCTTTGCCT 5413	5414	RESULT 3 US-09-129-112-13	; Sequence 13, Application US/09129112 ; Patent No. US2002001995A1 ; GENERAL INFORMATION: ; APPLICANT. Ft 71 or Marilyon F	APPLICANT: Murphy, Judith B.; APPLICANT: Murphy, Judith B.; APPLICANT: The Regents of the University of California TITLE OF INVENITION: A NO. US20020019995A1 Factor Binding Protein From Legume Roots	; CURRENT APPLICATION NUMBER: US/09/129,112; CURRENT FILING DATE: 1998-08-04; PRIOR APPLICATION NUMBER: US 08/907,226; PRIOR FILING DATE: 1997-08-06	NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin Ver. 2.1 SOFTWARE: Patentin Ver. 2.1 SERVETH: 1489		NAME/KEY: CDS LOCATION: (1)(1488)	NAME/KEY: CDS ; LOCATION: (43)(1413)	; OTHER INFORMATION: NBP46 US-09-129-112-13	Pred. No.: 1.12e-204 Length: 1489 Score: 1684.00 Matches: 319

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AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu 384
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                                                                                                                                                                GTCCATGTTTACCATTTTGATCAGAACTTAGATCTACTTCACATTGGCAATGATGATGAG 243
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                                                        67 ATCACTTCCTCCCAATATTTAGGAAACAACCTACTCACTAAT---CGAAAGATTTTCCAA
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47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerBrArg
                                                                                                                                              ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu
                                        LeuSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro
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APPLICANT: Etaler, Marilynn E.
APPLICANT: Etaler, Marilynn E.
APPLICANT: Etaler, Marilynn E.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
FILE REFERENCE: 023070-079810US
FURNET PILING DATE: 1998-08-04
PRIOR PILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VOS: 21
SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NOS: 19
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                                                                                 ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla 377
                                                                                                                                       CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal ---GluLysAspLys 396
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     CCTTGTCCCTATCAGAATTGCACTTTTGGTGGGATATGGAATGGTGGAGGTGGAAGTGGT
                                 GlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe
                                              LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly
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Patent No. US20020019995A1
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INFORMATION: full length
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| CTHER INFORMATION: NBP46
| NAME/KEY: modified base
| LOCATION: (1)..(1458)
| OTHER INFORMATION: n = g, a,
| US-09-129-112-8
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                     ProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLys 148
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                                                                                                          IleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAsp
                                                                        AlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyr
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Soreen, Steven E
APPLICANT: Tabask Jack E
APPLICANT: Tabask Jack E
APPLICANT: Tabask Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8688
IENGTH: 1483
 CTTCATCCAGTAGATTTCGAAATTGAAGCTAAGCGAGCTTGTGCATTAAACTTTGAGGAT 1143
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                       385 AlalysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-425-114-8688
                                                                                                                                                                                                                                                           Sequence 8688, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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1550.00
80.28%
64.25%
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Best Local Similarity:
Ouery Match:
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Pred. No.:
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Sequence 11084, Application US/10425114

Publication No. US2004003488A1

Publication No. US2004003488A1

Seprence 11084

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Application David K.

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Good Vongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENCE: 38-21(5313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
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                                                                                                                           SerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPheThrTyr
TyrvalHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgvalLysIlePheLysThr
                                                                                                                                                                     ThraspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSer
                                                                                                                                                                                      LeualaLeuGlnIleLeuargLeuasnGluProCysSerHisGluAsnCysThrPheGly
                                               ProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeu
                                                                 GluAlalleSerSerLeuProLysPheAsnArgLeuMetTyrPheIle 462
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US-10-425-114-11084
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                                                               APPLICANT: La COSCA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Thou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(33223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 2234
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Matches:
Conservative:
Mismatches:
Indels:
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                         Sequence 2234, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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80.48%
64.25%
64.48%
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Best Local Similarity:
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US-09-129-112-18
Sequence 18, Application US/09129112
Sequence 18, Application US/09129112
Sequence 18, Application US/09129112
Sequence 10, US2002019995A1
Sequence 10, US2002019995A1
Septemation: APPLICANT: Extler, Marilynn E.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US2002019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT ELING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
NUMBER OF FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
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1319 CTCSTGGAAGCAGCATGGCCACTAGGCGATGCCATAGAAGCCATATCATCATACCTAAA 1378
                         AsnGluProCysSerHisGluAsnCysThrPheGlyGlyIJIllTrpAspGlyGlyLysGly 336
         ProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316
                                                                                                                           337 SerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly
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1139 AAGGTTGCCTGTAACACAGAATTAAAGGATCTCAAATCCATTTTCCCTCGTGTTAAGGAT
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OTHER INFORMATION: DBX gene involved in oligosaccharide signaling
AMBEKET: sig_peride
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OTHER INFORMATION: DBX8 primer
NAME/KEY: primer bind
LOCATION: (297)...(314)
OTHER INFORMATION: DBX7-for/rev primer
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NAME/KEY: primer_bind
LOCATION: Complement((1)...(22))
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NAME/KEY: Primer bind
"ACATION: (274)...
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LOCATION: (61)..(1404)
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LENGTH: 1434
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Clone ID: 701006212_FLI
US-10-425-114-11084
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GluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAla
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Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: DEX11 primer
NAME/KEX: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: DBXbottom primer US-09-129-112-18
                                                       LOCATION: (688). (704)
OTHER INFORMATION: DBX2-for/rev pr.
NAME/KEY: primer_bind
LOCATION: Complement (766). (785)
OTHER INFORMATION: DBX10 primer
                                                                                                                                                                                                                                                                         LOCATION: (955). (972)
OTHER INFORMATION: DBX4 primer
NAME/KRY: misc feature
LOCATION: (1071). (1072)
OTHER INFORMATION: splice site
NAME/KRY: primer_bind
                                                                                                                                                                                                               OTHER INFORMATION: DBX5 primer NAME/KEY: primer bind LOCATION: (933)...(952) OTHER INFORMATION: DBX3 primer NAME/KEY: primer_bind
                                                                                                                                LOCATION: (856)..(857)
OTHER INFORMATION: splice site
NAME/KEX: primer_bind
LOCATION: (857)..(872)
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LOCATION: (856). (857)
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: HARDER, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Aun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIP1300-3
CURRENT FILING DATE: 2001-08-24
ERIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
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                           Sequence 87316, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated W
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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584 GCAGAAGCTGCTGTTCCTCAGGAGTTTCACCCCAGGACGCCAGTTAAACCTTGGAGCAACT
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49857C.1
US-10-424-599-87316
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1292.00
72.30%
53.91%
53.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Glycine max
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Query Match:
        US-10-424-599-87316
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LENGTH: 1784
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APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION NUMBER: US 60/2938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                    GluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPhePro 390
                                                                                                                                                                                                                                                                                                                                             AsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeu 410
                                                                                                                                                                                                                                                                                                                                                                                                    LeuvalaspGlyPheGlyLeuAspProGluGlnGluIleThrvalAlaGluGlyIleGlu 430
                                                                                                                                                                      GlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSer 352
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| OSI GGIGGICGAGGICAAAGAAIAIGITIGIIGCIICTITITITITITICGAICGIGCT
                GCCCTGCTTCACAATCGGGTGCGAGTCTTGACGAGTGCCGAAGGATAACCATCAACGCA
                                                                                                                                                                                                                              SerGluValGlyPheValThrPro-----ProAsnSerLysAsnArgProLeuAspPhe
                                                                                                                                                                                                                                              274 SerproCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn
                                                      294 IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle
                                                                                                               LeuàrgLeuàsnGluPro---CysSerHisGluàsnCysThrPheGlyGlyIleTrpAsp
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Matches:
Conservative:
Mismatches:
Indels:
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1281.50
74.15%
54.88%
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Query Match:
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US-09-938-842A-1888
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LENGTH: 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACAAAGCAGAAGCTTCTGTTCCCCGTGAGCTGCGTCCAAAGACACATGTCAGAGTTGGG
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                                                                                                                                                                                                                                                                                                             LeuLeuLeulleThrPheLeuLeuPheSerLeuProLysLeuSerSerGlnTyrVal
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242
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Mismatches:
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Matches:
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      PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                           ORGANISM: Arabidopsis thaliana
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1281.50
74.15%
54.88%
53.31%
                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                              ; ORGANISM: Arabic
US-09-938-842A-1888
                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                               SEQ ID NO 1888
LENGTH: 1419
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1   Gaps: 2   1	94 GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerleuIleProLeuLeu 113 331 GGGTGAGGGATATCCTACTGATCCCGAAGCAGCAAACTCTTTGGTGTCTCTTCTT 391 GGGTTGAGCGCATATCCTACTGATCCCGAAGCACAACTTTGGTGTTCTTTTTTTT	631 GGAAACCATACTCAGATACGGTAGGATGGTTGATCTTGGAGGGGGTCTGTTCAATG 690 214 AlaTyralavalSerArgAsnThralarysAsnAlaProLysProProGInGlyGluasp 233 214 AlaTyralavalSerArgAsnThralarysAsnAlaProLysProProGInGlyGluasp 233 31 GCATATGCTATATCTGAGGAAGATGCTGCAAGTGCCACAAACCATTAGAAGGAGAGGAT 750 234 ProTyrMetLysLysLeuValleuLysGlyVsLysTyrAspleuTyrValHisSerTyr 253 334 ProTyrMetLysLysLeuValleuLysGlyVsLysTyrAspleuTyrValHisSerTyr 253 335 TCATATGTCAGAGAGATGTATCTGAAGGACGGAAGTATTTCCTCTATGTTCACAGTTAC 810 254 LeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThThraspGlyAlaAla 273 336 TCACATTACGGATTACTGGAGCGCTCGAGCAGATTTTGAAAGTTTCTGAAGATTACTGAAGATTCTGAAGATTCTGAAGATTCTGAAGATTCTGAAGATTACTGAAGATTCTGAAGATTCTGAAGATTCTGAAGATTCTGAAGATTCTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTGAAGATTACTAGATTACTAGAAGATTACTAGAAGATTACTAGAAGATTACTAGAAGATTACTAGAAGATTACTAGATTAGAAGATT	274 SerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293 3.::           :::::            :::

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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION WIMBER: US 60/22, 866
FILE REPERENCE: 2001-08-24
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/20,111
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: OF SEQ ID NOS: S379
SEQ ID NO 849
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                                  GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly
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   ; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-01-6
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 849
; LENGTH: 1416
                                                                                                                                                        TYPE: DNA ORGANISM: Arabidopsis thaliana
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: And APPLICANT: SCATTAINION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Buchkarov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEG ID NOS: 204966
SEQ ID NO 29868
LENGTH: 2071
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                                            274 SerproCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn
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US-10-437-963-29868
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Roberts,N.J., Brigham,J., Wu,B., Murphy,J.B., Volpin,H.,
Phillips,D.A. and Etzler,M.E.
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Roberts, N.J., Brigham, J., Wu, B., Murphy, J.B., Volpin, H. Phillips, D.A. and Etzler, M.E.
A Nod factor-binding lectin is a member of a distinct c apyrases that may be unique to the legumes
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AF156782. GI:6006798
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1 (bases I to 1458)
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2 Etzler,M.E. and Murphy,J.B.
Nod factor binding protein from legume roc
AL Patent: US 6465716-A 8 15-00T-2002;
1 Location/Qualifiers
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Matches:
Conservative:
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                                                                               GTTAACTATGGGGGAATTGGGAAAAGCTTCACAAAATCAGTGGGAGTAATTGAC
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db_xxef="G1:6006799"

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VCCDLLYQHVLLVHGFGLGFRKEITVGEGIQYQNSVVEAAMPLGTAVEAISALPKFKR
                        Biology, University
CA 95616, USA
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Indels:
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phosphohydrolase"
                                                                                   organism="Medicago sativa"
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                                                                                                                       ProlysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla
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            Avarage declaration of the Apyrase-Like APY1 Genes in Roots of Medicago Expression of the Apyrase-Like APY1 Genes in Roots of Medicago Structucatula Is Induced Rapidly and Transiently by Stress and Not Sinorhizobium meliloti or NoG Factors Plant Physiol. 131 (3), 1124-1136 (2003)

2 (bases 1 to 1466)

Cullimore, J. V. and Niebel, A.

Direct Submission

Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan 31326, France
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE TOTIENAL	PUBMED REFERENCE AUTHORS TITLE JOURNAL	FEATURES source	gene		polya_ ORIGIN	Alignment Score Pred. No.: Percent Similar Best Local Simi Query Match: DB:	OY Db	2

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LEQAEDVVPDDLQPKTPVRLGATAGLRLLNGDASEKILQSVRDMLSNRSTFNVQPDAV
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ADGDDPYIKKVVLKGIPYDLYVHSYLHFGREASRABILKITPRSPPCLLAGFNGIYT
YSGEBERATAYTSGANFNKCKNTIRKALKLAYPCPYQWCTFGGIWNGGSGNQGNLFA
SSSFFYLDEDTGWVDASTPNFILRPVDIETKAKEACALNFEDAKSTYPFLDKKNVASY
VCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALDRKFER
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protein_id="BAB40230.1"
db_xref="G1:1348667"
/translation="MEFLIKLITFLLPSMPAITSSQYLGNNLLTSRKIFLKQEEISSY
                                            1410
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clone:pKS5-1.
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               457
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Subbta,K., Morita,Y., Abe,S., Stankovic,B. and Davies,E.
Apyrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of
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                          1351 CCTCTAGGGAATGCTGTAGAAGCCATATCATCGTTACCTAAATTTGAACGAATGATGTAT
               ProLeuGlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyr
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Plant Physiol. Biochem. 37, 881-888 (1999)
2 (sites)
2 Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of gene from pea (thisum sativum)
Acta Physiol. Plant. (2001) In press
3 (bases 1 to 1648)
Shibata,K. and Abe,S.
Direct Submission
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Pisum sativum mRNA for S-type apyras, complete cds,
AB027613
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/strain="Alaska"
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AVYEDAGSTGGRIHVHENQUIDLEHIGKGYBYYNKITPGLGSYANDPEQAKSLIBY
LEQAEDVVPDDLOPKTPVRLGATAGLELHIGKGYBYYNKITPGLGSYANDPEQAKSLIBY
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Pisum sativum mRNA for apyrase, complete cds, clone:pKS17-2.
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Submitted (12-FEB-2000) Shunnosuke Abe, Ehime University, College Submitted (12-FEB-2000) Shunnosuke Abe, Ehime University, College of Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan (E-mail:abe@mcb.agr.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp, Tel:+81-89-946-9853,
Fax:+81-89-946-9853)
                                                                IleTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAla
                                                                                   1049 TACCTACCTGAAGATACCGGTATGGTTGATGCAAGCACACCTAATTTCATACTTCGGCCG
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IleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPheGlyGly
                    TyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisPro
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/tissue type="bark grown stem internode"
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/organism="Pisum sativum"
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                                      pea treated elicitor"
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Mismatches:
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from I
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Matches:
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1. .1660
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Submitted (10-5EP-2001) Tomonori Shiraishi, Okayama University;
1-1-1 Tsushima naka, Okayama city, Okayama 700-8530, Japan
(E-mail:tomoshir@cc.okayama-u.ac.jp, Tel:81-86-251-8311,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophy
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae,
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 AsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGly
                                                                 ValglualaileseralaleuprolysPhelysArgLeumetTyrPheile 459
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COMMENT OS Pisum sativum L. (Garden Pea)  BN JP 2001017176-A/1  BN JP 200101716-A/1  BD 23-JAN-2001  PF 02-JUL-1999 JP 1999189129  PR TOMONORI SHIRAISHI, IWAO FURUSAWA  PC 012N15/09, A01H5/00, C07K14/415, C12N9/16, C12N15/00 CC  FH Key I. al368  FT Source /organism='Pisum sativum L. (Garden Pea)'.  FEATURES I. al368  /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"	Alignment Scores: Pred. No.: Social: Pred. No.: 1769.00 Matches: Score: Score: 1769.00 Matches: Score: Scor	Db   58 TCCTCCCAATACTTAGGAAACATCTACCAGTAGAAAGATTTTCCTAAAACAAGAG   117	
Db 567 TTGGGAAATTTAGGGAAAAAGTACACAAAAACGTTGGAGGTAATAGATCTTGGAGGTGCA 626  Qy 205 ServalGlnMetThrTytAlaValSerLysLysThrAlaLysAsnAlaProLysValAla 224  C25 AFGGTTCAAATGGGCTAACAGAAAAACTGCTAAAAATGCTCCAAAAGTTGCA 686  Qy 225 ASGGJYGLUASPPROTYTILELYSLYSLEUVALLeuLySGJYLYSGLNTYRASDLEUTYR 244  [	ACACA	110 110 110 110 110 110 110 110 110 110	Db 1284 GGGAAGGAAATGAATACGAATCCTATTCTGGAAGCTGCTGCTGCTTTTTTTT

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Conservative:
Mismatches:
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Submitted (24-MAY-1999) Shunnosuke Abe, University of Ehime,
Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime
790-8566, Japan (E-mail:abe@dpc.ehime-u.ac.jp,
URL:http://wbb-mcb.agr.ehime-u.ac.jp/bunnshi/, Tel:81-899-46-9853,
Fax:81-899-46-9853)
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 GATGGAGATGATCCATACATCAAGAAGGTTGTACTCAAGGGAATACCATATGATCTTTAT
                                                   ValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThr
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Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of
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Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1572)
Shibata,K. and Abe,S.
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Structure of the coding region and mRNA variants of the apyrase from Pisua Sativum.
Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1645)
Shibata, K. and Abe, S.
Direct Submission
Submitted (12-7AN-1999) Shunnosuke Abe, University of Ehime,
Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime
UNL:http://web-mcb.agr.ehime-u.ac.jp,
Fax:81-899-46-9853)
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 GTTTCTATAATTGATGGAACCCAAGAAGGTTCTTATCTATGGGTGACAGTTAACTATGCA
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                                                                                                                                   ValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThr
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AVVEDAGSTGSRIHVYHENONLDILHIGKGVEYYNKITPGLS SYANNPEQAAKSLIFL
LEQAEDVVPDDLQPKTPVYRLGAHAGIELLNGORSEKILGVSYRDMLSNRSTFRVVQDDAV
SIDGTQBGSSYLMYVYNYALGAHGIEKKYTKYTGVIDLGGGSVQMAXNSKKTRANAFKA
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29. 1396
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/standard name="ATP diphosphohydrolase"
/note="cytoskeleton associated"

/organism="Pisum sativum

/mol\_type="mRNA" /cultivar="Alaska"

Location/Qualifiers

1. .1645

/db\_xref="taxon:3888" /clone="pKS23-4"

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Mismatches:
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85.56%
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LMYFV"
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Best Local Similarity:
           transit_peptide
polyA_signal
                                                                   Scores:
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PLN 20-MAR-2001

linear

AB022319 1645 bp mRNA li: Pisum sativum mRNA for apyrase, complete cds. AB022319

AB022319.1 GI:4519172

apyrase.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

LOCUS

pisum sativum (pea)
pisum sativum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids; eurosids I, Fabales; Fabaceae; Papilionoideae, Vicieae,

1 (sites) Shibata, K., Abe, S. and Davies, E.

Pisum

REFERENCE AUTHORS

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unkwa linear PLN 20-MAR-2001
complete cds, clone:pKS30-3.
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                                                                                                                                                                                   Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of the apyrase from Pisum Sativum

Acta Physiol. Plant. 20, 3-13 (2001)

Acta Physiol. Plant. 20, 3-13 (2001)

Shibata,K. and Abe,S.
Direct Submission

Submitted (22-FBB-2000) Shunnosuke Abe, Ehime University, College of Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan (B-mail:abe@mcb.agr.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp,
Fax:481-89-946-9853)

Location/Qualifiers
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                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="pisum sativum"
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/db_xref="taxon:3888"
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/clone="pies"pk30-3"
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                       Pisum sativum mRNA for apyrase,
         1648 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Seedling
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                                                   AB038669.1 GI:11596082
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         AB038669
                                        AB038669
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                                                        LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIle 144
                                                                                       445
                                                                                                                   LeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAla 164
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RESULT 11 AB038669

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SIIDGTOGGSYLMVTVNYALGNLGKRYTKTVGVIDLGGGSVQMAYAVSKKTARNAPKA
                                                                                                                                                                                                                                                                                            Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Vicieae;
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YSGEBFKATAYTSGANFNKCKNTIRKALKLNYPCPYQNCTFGGIWNGGGGNGQKNLFA
SSSFFYLPEDTGMVDASTPNFILRFVDIETKAKEACALNFEDAKSTYPFLDKKNVASY
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                        GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla
                                             Submitted (21-APR-1994) Hsieh H., University of Texas at Austin, Botany, Biological Lab. Rm 6, Austin, Texas, USA, 78713
                                                                                                                                                                                             bp mRNA linear PLN 04-JI
WA for nucleoside triphosphatase.
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Hsieh, H.L., Tong, C.G., Thomas, C. and Roux, S.J.
Light-modulated abundance of an mRNA encoding a
calmodulin-regulated, chromatin-associated NTPase in pea
Plant Mol. Biol. 30 (1), 135-147 (1996)
                                                                                           ValGluAlalleSerAlaLeuProLysPheLysArgLeuMetTyrPhelle
                                                                                                            transport
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/clone_lib="pea plumule c'
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1. .1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Pisum sativum"
                                                                                                                                                                                                                                                                triphosphatase
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NTPase, nucleoside
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GAAATTTCCTCTTACGCTGTAGTATTCGATGCTGGTAGCACCGGTAGTCGCATTCATGTT 205
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                                                 386 GTTAGACTTGGGGCAACTGCCGGTTTAAGGCTTTTGAATGGAGATGCTTCTGAAAAGATA
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                               TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
                                                                                                LyslleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu
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866 GAAGAGITTAAGGCAACTGCTTACACTTCTGGTGCAAACTTTAATAATGCAAAAACACA
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                                                                              IleTrpAsnGlyGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAla
                                        942 Africgiaagecicifiaagingaactarccffgfccarafcagaarfgcactfffgga
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Mismatches:
Indels:
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/citation=[1]
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen fixation; fertilizer; ss.
                                      Abz42130 Ada68447 Abz13044 Ada68468 A
                                                                                              Ada69716 F
Ada71114 F
Ada71114 F
Aax08523 N
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Ac119006 I
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/product= "NBP46 root lectin"
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Medicago sativa.
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-Q=/cgn2_1/USPTO spool/US09657631/runat_10082004_171045_1662/app_query.fasta_1.1294
-Q=/cgn2_1/USPTO spool/US09657631/runat_10082004_171045_1662/app_query.fasta_1.1294
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-LOOPEXT=0 -UNITS=bits -CFNAT=1 -END=-1.—MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_NIN=0 -ALIGN=15
-MODE=LOCAL_OUTFNT=ptc -NORM=xt -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=LOCAL_OUTFNT=ptc -NORM=xt -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=LS09657631_GCGS1_1_L687_GCN=10082004_171045_1662 -NCPU=6 -ICPU=3
-NO MMAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPENOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPPOP=6
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Aaf85681 Pea bligh
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                        nucleic search, using frame_plus_p2n model
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production of transgenic plants which are able to fix nitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding Lotus japonicus lectin/nucleotide phosphohydrolase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lectin/nucleotide phosphohyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein, nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth; plant development; antisense technology; gene; ds.
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introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nuclectide phosphotytolase) polynuclectide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, at suspected to be involved in binding a variety of carbohydrates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynuclectide), resulting in increased uptake of nutrients by plants and better growth/development, but antisense for other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Lotus japonicus lectin/nuclectide phosphohydrloase (LNP) that can be used to modulate mycorrhizal infection in plants. (Updated on 29-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes a method of modulating mycorrhizal infection
                                                                                                                                                                                                                                                                                                                                                                                   Modulating mycorhizal infection, useful for improving plant growth, transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
            "Lectin/nucleotide phosphohydrolase"
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P-PSDB; AAU78819.
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                          GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla
                                            241 GAGTITGTGACAAGATCAAACCAGGTITGAGTGCATATGGGGATAATCCTGAACAAGCA
                                                                                 101 AlaLysSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHis
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                            LeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAla
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              459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New blight-resistant polypeptide useful for giving blight resistance
             ThralavalGlualaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
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                                                                                                                                                 Pea; blight resistance; nucleotide triphosphate decomposition;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                             resistance protein coding sequence #1
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                                                                       AAF85679 standard;
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Best Local Similarity:
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                                                                                                                                                                     Pisum sativum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 ValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCysLysGlu1le 304
                                                                                                                   IleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro
                                                                                                                                                                                                                                                                                                                                                                                     522 GTTTCTATAATTGATGGAACCCAAGAAGGTTCTTATCTATGGGTGACAGTTAACTATGCA
                                TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
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                                                                                                                                                                                     LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIle
                                                                                                                                                                                                                                                                402 GTTAGACTTGGGGCAACTGCCGGTTTAAGGCTTTTGAATGGAGATGCTTCTGAAAAGATA
                                                                                                                                                                                                                                                                                                 LeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAla
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                                                                                                                                                                                                                                                                                                                     ValSerIlelleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 IleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPheGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 IleTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1062 TACCTACCTGAAGATACCGGTATGGTTGATGCAAGCACACCTAATTTCATACTTCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 AsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 ValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAspPheGluAspValLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrTyrProArgLeuThrAspAlaLysArg-----ProTyrValCysMetAspLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells by altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It is useful for increasing the sensitivity of cells to chemcheraputic and antibiotic agents and increasing resistance to herbicides. The present sequence is from Pisum sativum and encodes an ecto-phosphatase (extracellular phosphatase). This sequence was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the Specification, but is referred to via its GenBank accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells comprises altering ATP gradient across biological membrane of target cell.
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                         chemotheraputic;
          ValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
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                                                                                                                                                                                                                                             resistance; ATP gradient; chextra-cellular phosphatase;
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Matches:
Conservative:
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                                                                                                                                                                                                          Ecto-phosphatase coding sequence
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                                                                                                                                                                           (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1999;
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                                    65 TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
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                                               The present invention provides the protein and coding seguences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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                                                                                            Pea; blight resistance; nucleotide triphosphate decomposition;
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       GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGlnLysGlnGlu 44
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                       ThrLeuThrSerIyrAlaValllePheAspAlaGlySerThrGlyThrArgValHisVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New blight-resistant polypeptide useful for giving blight resistance
                                                                                                                                                                                                                                                          Pea; blight resistance; nucleotide triphosphate decomposition; ds.
                                                                                  GTAGAAGCCATATCAGCTTTACCTAAATTTGAGCGATTGATGTATTTTGTT 1406
                                                             ValGluAlalleSerAlaLeuProLysPheLysArgLeuMetTyrPhelle 459
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62
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                Pea blight resistance protein coding
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25. .1392
/*tag= a
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                                                                                                                                               AAF85680 standard; DNA; 1697 BP
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                                                                                                                                                                                                                LysasnWetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMetProAla
                                                                                                                                                                                                                                   41 GlnLysglngluThrLeuThrSerTyrAlaValIlePheAspAlaglySerThrGlyThr
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                                                                                        Conservative:
Mismatches:
 444
                                                    Length:
Matches:
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 324
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 437 A; 284 C;
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                                                      5.48e-159
1665.50
83.04%
68.70%
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   BP:
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   Sequence 1489
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                                         1338
     442
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                          GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla
                                                                                                                                                                                                                                                                                             LNP.
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                                                                                                 DNA encoding Medicago sativa lectin/nucleotide phosphohydrolase,
                                                                                                                                                                                                                                                                                                                             Lectin/nucleotide phosphohyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein; nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth; plant development; antisense technology; gene; ds.
                                                                            ValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "LNP"
/note= "Lectin/nucleotide phosphohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "No start or stop codon given"
/rransl_except= (pos:22. .24, aa:Xaa)
/rransl_except= (pos:1411. .1413, aa:Xaa)
/rransl_except= (pos:1453. .1455, aa:Xaa)
/note= "Xaa= Stop codon"
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P-PSDB; AAU78820.
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The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, expression of NBP46 can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
                                                                                                                                                                                                                                                                                                                                                                                                rhizobial bacteria via a lectin-carbohydrate interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261
                                                                                                                                                                                                                                                                                                                                              LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 AACCAGGAACTCCTTACCTCTTACGCTGTCATCTTTGATGCTGGTAGCTCTGGGAGTCGT
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                                                                                                                                                                                   1111 AAAATTGGTCCAGTTGATTTGAAGACTGCAGCTAAACTAGCTTGTAAAACAAATCTTGAG
                                                                                                                                                                                                             381 ASPValLysSerThrTyrProArgLeuThrAspAlaLysArg---ProTyrValCysMet
CysLysGluIleIleLeuLysValleuLysValAsnAspProCysProTyrProSerCys
                         934 IGCAGAAAGAIAGCTCITAAGGCTCTTAAAGIGAATGCACCTTGTCCCTATCAGAATTGC
                                                                                                     SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer
                                                                                                                       1054 TCATCTTTCTATACTCTCTGAAGATGTTGGG---ATCTTTGTGAATAAACCCAATGCC
                                                   ThrPheGlyGlyIleTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThr
                                                                      994 ACTITIGGIGGGATATGGAATGGIGGAGGIGGAAGIGGICAAAAAAAATCTTTCCTTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LysasnMetGluPheleulleThrLeullealaThrPheleuLeuLeuMetProAla
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                    06-SEP-2001;
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14-MAR-2002
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                                                                                      AlapheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIle
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 GACCTTTATGTTCACAGTTACTTGCGTTATGGTAACGACGCAGCACCAGCACGTTAAAGATTTT
                                 AsnalaThrasnGlySeralaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr
                                            TyrserglyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCys
                                                                                                                LysGlullelleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr
                                                                                                                                                        PheGlyGly11eTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                   Dolichos biflorus lectin/nucleotide phosphohydrolase,
                                                                                                                                                                                                                                                                                                                                                                                                        AlavalGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lectin/nucleotide phosphobyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein; nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth; plant development; antisense technology; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Lectin/nucleotide phosphohydrolase"
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195. .1436
/*tag= c
/label= Mature_LNP
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Conservative: Mismatches: Indels: Length: Matches:

8.23e-158 1654.50 82.75% 67.03%

Gaps: (1-1643)

x ABK11098

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The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide phosphorytolase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in olingosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but antiense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Dolichos biflorus lectin/nucleotide phospholydrloase (LNP) that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating mycorhizal infection, useful for improving plant growth, transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
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2001WO-US028165
                                                                                      06-SEP-2000; 2000US-00657631
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1143 AATCGCCTCTGGATTTTGAAACTGCAGCTAAACAAGCTTGTAGTTTAACATTCGAGGAA 1202
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|Aaaccacaaaggagaggatcatacatgaagaagcttgtactcaagggaaagaatt
                                                                                                                                                                                               GluLysileLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln
                    489 GAAAAGATATTGCAAGCGGTTAGGGAAATGTTCAGGAACAGAAGTTCCCTGAGCGTTCAA
                                                 AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeu
                                                                                    LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr
                                                                                                                                                                                                                        262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr
                                                                                                                                                                                                                                162 ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
                                                                                                             GlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro
                                                                                                                                                                                                                                                                        LysGluIleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr
                                                                                                                                                                                                                                                                                                                                                                    AlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIle
                                                                                                                                                                                                                                                          TyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCys
                                                                                                                                                                                                                                                                                                        CGTGACCTACAGCTCTCAGATTCTCAGATTGAGCCATGTTCCCATGAAAACTGCACC
                                                                                                                                                                                                                                                                                                                                PheGlyGlyIleTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSer
                                                                                                                                                                                                                                                                                                                                                                                                        362 LeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAsp
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transpenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
                                      NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen; nitrogen; ss.
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production of transgenic plants which are able to fix nitrogen.
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively,
                                                                                                                                                                                                                               NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
                                                                             400 AspleuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGlu
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                                                                                                                                                                            GlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
  361 IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu
                           1111 AAAATTCGTCCAGTTGATTGAAGACTGCAGCTAAACTAGCTTGTAAAACAAATCTTGAG
                                                     AspVallysSerThrTyrProArgLeuThrAspAlaLysArg----ProTyrValCysMet
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expression of NBP46 can be used to modulate oligosaccharide signalling in the plant. The mucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene expression. This DBX sequence also isolated from D. biflorus is also involved in oligosaccharide signalling
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             844 TCTGGTTTTGATGGGTATTACACATACGGAGGAGTCCAGTATAAAGCCACAGCTCCCCCT
                                          SerGlySerAsnPheAspAspCysLysGluIleIleLeuLysValLeuLysValAsnAsp
                                                          354 GluProAsnLysProAsnSerIleLeuHisProValAspPheGluIleGluAlaLysArg
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1084 GATCCAAACGAIGCCAAIGCCAIAGTICGTCGIGGAITITIGAAGAIGCAGAAAGGIT
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                        the invention targets of comprising; (a) contacting nucleic acid may been exposed, comprising; (a) contacting nucleic acid mit representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the plant of a stress response. The method is useful in the plants with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                       invention relates to identifying a stress condition to which a plant
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GTTGAAGAGTATTCTGTGCATAATCGCAAAGGAGGTCCTAATTCGAGAGGTCCGAAGAT
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         plants with increased tolerance to these abiotic stresses
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The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell and expressing the nucleic acid segment in for augmenting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell, to produce a differentiated transformed plant transformed shown in ABZ42017 - ABZ42142 represent segments of A. thaliana cDNA modulated by PTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 ATTGTGTTGATCGGTCTCGTTCTTCTGCTATGCCTGGGAGATCGATTTCTGATTCCGTC 150
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                                                                                                                                       Novel polynucleic acid segment useful for modulating within a cell by posttranscriptional gene silencing, plant cell genome.
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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                                                                                                                                                                                                                  Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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ArgasnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle
            GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlyGlySerValGlnMet
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                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                                    Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 information supplied to Derwent by the Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                         Claim 144; SEQ ID NO 849; 577pp + Sequence Listing; English.
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                          thaliana; plant; gene; stress; transgenic; ds
 Arabidopsis thaliana stress regulated gene SEQ ID NO
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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22-JUN-2001; 2001US-0300111P
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                                                    Arabidopsis thaliana
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Best Local Similarity:
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                        Arabidopsis
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GlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro

868 CAGAATTTGGATCTTTGTTTGGAGAATGAGCTCGAGCTCTTTACAGCTAAAACCG

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TyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp

148 GTCATCGAGTACACGATGAAAAACCACGAGGAGGTTCCAATTCGAGGGGTCCGAAGAAT

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                                  AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr
                                                                                                                        508 AGGGAGCTCCTCAAAGGTAGAAGTAGGCTGAAGACTGAGCCAAATGCAGTGACTGTTCTG
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                                                                 448 GCAACTGCAGGTTTGAGAGCTTTGGGTCACCAAGCCTCTGAAAACATTTTTGCAAGCGGTT
                                                                                                  ArgasnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle
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Search completed: August 19, 2004, 15:28:07 Job time: 540.788 secs

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GenCore version 5.1.6
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- nucleic search, using frame\_plus\_p2n model OM protein Run on:

August 19, 2004, 14:05:21; Search time 3544.42 Seconds (without alignments) 3867.136 Million cell updates/sec 1 OIKNMEFLITLIATFLLLLM......GTAVEAISALPKFKRLMYFI 459 US-09-657-631-4 Title: Perfect score:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 Scoring table: Sequence:

27513289 seqs, 14931090276 residues Searched:

55026578 of hits satisfying chosen parameters: Total number

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE=7

ESI:\* Database

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em\_estin:\*
em\_estmu:\*
em\_estov:\*
em\_estol:\* em\_estro:\* em\_htc:\* gb\_est1:\* gb\_est2:\* gb\_htc:\* gb\_est4:\* gb\_est5:\* em estba:\* gb\_est3:\* 10;

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em gss vrt:\* em\_gss\_fun:\* mam:\* em\_estfun:\* 

em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* \*:snw em\_gss\_pro:\* em gss

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result	Sco	re	Query Match	Length	DB	ID	Description
1 4 4	1	•	1	1.	-		
	Н	_	44.9	9	12	G58441	4413 EST486
	1000	•	ĸi.	4	12	64448	G644489 EST506
	991	•	÷.	743	13	16519	Q165194 EST611
	σ	ויי	ė.	LO	10	00384	F003844 EST432
	6	CA	œ.	v)	12	BI267324	67324 NF105
	æ	w	۲.	ന	13	25541	Q255419 MTNAL8
	œ		ė.	ശ	12	26310	I263104 NF038F
	00	œ	ė	ເກ	12	27038	70380 NF010D
	œ	o.	ġ.	വ	10	58459	34590 N21066
	œ	ഗ	ď.	_	13	14841	48414 NF068A1
	80	LO.	ņ.	$^{\circ}$	12	BI272922	72922 NF091F0
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	e B	₹"	'n.	n	12	26573	I265733 NF093B1
	8	マ	'n	o	10	32570	B325702 NF055F1
	5 834		س	വ	12	45747	3457472 NF106A0
	824	•	4.	₩	12	26535	I265356 NF093G1
	7	N.	4.	ഹ	12	4901	G449019 NF003H0
	80	$^{\circ}$	4,	n	12	5769	3457694 NF10
•	80	CV.	4.	o	12	95	66953 NF098A0
•	8	$^{\circ}$	4.	LO.	10	4162	F641625 NF065A0
- •	1 8	$\overline{}$	4.	LO.	10	79	41795 NF067E0
. •	2 818		4.	9	12	5732	I267321 NF105
•	3 816		4	4	12	1984	49843 NF053
•	æ	←	₹.	ന	10	1130	41307 NF051D0
. •	80	0	œ.	I.O.	10	3916	39165 NF094
	œ :	0	ë.	IO.	12	5349	53495 NF086
. ,	7 800		m.	In.	13	1636	46365 NF047
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. •	793	•	· ·	m	12	5509	55090 NF004
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		ν.	n	n.	17	27133	71332 NF020D1
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7'		7	~:	$\sim$	12	6768	682 NF111F08
7	7	7	٠. د	^1	10	F64243	F642432 NF063E04
7	7	9	٠. ما	583	10	E32287	E322878 NF048
7	3	9	٠. ما	_		126770	I267700 NF113G12
4.	7	9	٠ <u>.</u>	$\sim$ 1		5529	55293 MTNAF12T
7	16	•	<u>،</u>	624		E32210	E322109 NF010B12

## ALIGNMENTS

EST486173 MHAM Medicago truncatula/Glomus versiforme mixed EST ll-APR-2001 library cDNA clone pMHAM-15D7 5' end, mRNA sequence.
BG584413.1 GI:13599477 DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BG584413

Medicago truncatula/Glomus versiforme mixed EST library Medicago truncatula/Glomus versiforme mixed EST library Eukaryota, mixed EST libraries.

1 (bases 1 to 760)

Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.

REFERENCE AUTHORS

ORGANISM

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/note="Vector: pBluescript SK -; Site 1: BcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUO44449 745 bp MRNA linear EST 24-APR-2001
EST506108 KV3 Medicago truncatula cDNA clone pKV3-37M24 5' end,
MRNA Sequence.
                                                                                                                                                                                                              548
                                                                                                                                                                                                                                                                                                                                                                                                                      228 pProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTy 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                    169 AspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeu
                                                                                                                                                                                                                                                        208
129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
                                                                                                                             488
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mellloti"
                                                                                                                                                                                               489 GATGGAACCCAAGAAGGTTCTTATCTCTGGGTGACAGTTAACTATGCATTGGGAATTTA
                                                                                                                                                                                                                                                                                  tThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAs
                                       369 GCAACCGCAGGTTTAAGGCTTTTGAATGGGGATGCTTCTGAAAGATATTGCAAGCGGTA
                                                                                     149 ArgasnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle
                                                                                                           189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGly-GlyGlySerValGlnMe
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VandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D.,
VandenBosch, K., Endre, G., Hur, J., and Fraser, C.M.
Esys from roots of Medicago truncatula 72 h after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M392896e TIGR sequence name: MTEBP84TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     St. Paul, MN 55108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab host="E. coli strain XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTACACTTTGGTAGAAAGCATCTCGAGCT 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Plant Biology
University of Minnesota
220 BioScil Center, 1445 Gortner.
Tel: 612 624 2755
Fax: 612 625 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inoculation, 2001
Unpublished (2001)
Contact: VandenBosch K
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library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note—Tecor. Bluescript SK-; Site 1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days sost-inculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 GlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages." /lab_host="%" coli strain XLOLR" /clone_lib="WHAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 TTAGGAAACAACCTACTCACTAATCGAAAGATTTTCCAAAAACAAGAAAAATTTCCTCT 128
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                     ESTs from roots of Medicago truncatula after colonization with Glomus versiforme, 2001
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                          Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-221-7380
Rax: 580-221-7380
Noble EST name: N379883e TIGR sequence name: MTDBQ16TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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44.88$
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               Fraser, C.M.
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Van Aken, S.

USA

55108,

More

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/clome_lib="KVKC"
hote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/hof: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 SerSerGlnTyrLeuGlyAsnAsn---LeuLeuThrAsnArgLysIlePheGlnLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValTyrHisPheAspClnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheVal
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                                                                                                                                                1 (bases 1 to 743)
VandenBosch, K., Endre, G., Silverstein, K, Town, C.D., Van Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected re-arrayed from various libraries
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                       Tel: 612 624 2755
Fax: 612 625 1738
Fax: 612 625 1738
Email: kvandenbecbs.umn.edu
TIGR sequence name: WTNAF77TK Alias Clone name: KV2-6L1
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                         Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MV
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Mismatches:
Indels:
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                                                                                       Eukaryota; Viridiplantae; Streptophyta;
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/dev stage="various stages"
/lab_nost="XLOLR"
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Matches:
                                                        Medicago truncatula (barrel medic)
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                         GI:20307369
                                                                                                                                                                                                                                                         Contact: VandenBosch K
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                                                                          truncatula
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89.11%
80.24%
41.59%
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                        BQ165194.1
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Best Local Similarity:
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                                                                      Medicago
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DB:
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                                                                      ORGANISM
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                                                                                                                                                       REFERENCE
AUTHORS
        ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                         COMMENT
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EST611063 KVKC Medicago truncatula cDNA clone pKVKC-6G5, mRNA
sequence.
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing ofbM inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells.
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Matches:
Conservative:
Mismatches:
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1000.50
89.92%
79.44%
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                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                Percent Similarity
                                                                                                   Scores:
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                                                                                                                 Pred, No.:
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173

83

63

43

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BI267324

NF105B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone NF105B12IN 5', mRNA sequence.
                                                         /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using digapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp 300
/dev stage="24 hours post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                        421 ACATATTCAGGAGTGGAGTACAAGGCTTTTTCCCCTTCTTCTGGCTCAAACTTTAATGAA
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178
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Indels:
                                   /lab host="E. coli strain XLOLR"
/clone_lib="KV1"
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Matches:
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Medicago truncatula
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Best Local Similarity:
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More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. 0556
                                                                                                                                                                                                                                                                                      203
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                   ProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLyS 143
                                                                                                                                                                163
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Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
                                        123
                                                                      353
                                                                                                                     BSTs from roots of Medicago truncatula 24 hours after inoculation with Sinorhizobium meliloti Unpublished (1999)
Contact: VandenBosch K
           293
                                                         GlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                AlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeu
                                      Leulle ProLeuLeuGludladlagludspyal Val ProGludspLeufis ProLysThr
                                                                                                                                                                  IleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAsp
                                                                                                                                                                                                                            AlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyr
                                                                                                                                                                                                                                                       GCAGTTTCTATTATTGATGGAACCCAAGAAGGTTCTTATCTCTGGGTGACAGTTAACTAT
                                                                                                                                                                                                                                                                                       184 ValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGly
                                                                                                                                                                                                                                                                                                                    534 GCATTGGGGAAATTGGGAAAAATTCACAAAAACAGTGGGAGTAATGGATCTTGGAGGT
         AATAAGACAACGCCCGGTTTGAGTGCATACGCGGATAATCCAGAAGAAGCTGCAAAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/mol type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV1-13H12"
/tissue_type="Seedling roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGLICATAGGTACTTACACTTT 737
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Fax: 612 625 1738
Email: kvandenb@ch
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Conservative:
Mismatches:
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/dev_stage="various stages"
/lab_host="XLOLR"
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/clone="pKVKC-12G8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                               BQ255419
MTNAL80TKM KVKC Medicago
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BQ255419.1 GI:20456172
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Fax: 612 625 1738
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/folome_lib="Insect herbivory"
/note="Vector: Lambda Zap, Library was produced from fully
sexpanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
                   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
   Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 yAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeuGluGluAlaGluAspVa 114
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                                                                             Korth, K., Soct, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 AlaGlySerThr-GlyThrArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GCTGGTAGCACCTGGAAGCCGTGTCCATGTTTACCATTTTGATCAAAACTTAAAATCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uHisIleGlyAsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 lValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="local and systemic leaves"
/dev_stage="mature"
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177
19
19
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Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR
Pax: 501 575 5191
Email: kkorth@comp.uark.edu
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/mol_type="mRNA"
/db xref="taxon:3880"
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                   Insert Length: 651 Std Error: 0.00 Plate: 105 row: B column: 12 Seg primer: TCACACAGGAAACAGCTATGAC. Location/Qualifiers
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/clone_TVEVEC.
/clone_TVEVEC.
/note=TVECTOR: BBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; CDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
strates. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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VandenBosch,K., Endre,G., Silverstein,K., Town,C.D., Van Aken,S.,
Utterback,T., Cheung,F., Fraser,C.M., Lamblin,A.-F. and Retzel,E.F.
The Medicago truncatula 'kiloclone' set; A selection of ESTs from
Various libraries rearrayed for gene expression studies
Unpublished (2002)
                                                                                                                                                                                                                                                                                           234
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                                                                              481
                                                                                                                                                                                                                                                                                                                                     542 GTATACAGCTAAAAATGCTCCAAAAGTTGCTGATGGAGAAGAACATCCATACATTAAGAAGCT 601
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This sequence represents the 5' end of the cDNA insert. More
information is available at: www.medicago.org
Seq primer: 5'9GT CTT AgA ACT AGT ggA TC 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               735 bp mRNA linear EST 06-MAY-;
truncatula cDNA clone pKVKC-12G8, mRNA
174 yserTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLy
                                     422 TTCTTATCTCTGGGTGACAGTTAACTATGCATTGGGGAAATTGGGAAAAATTCACAAA
                                                                                                                                                                               214 sLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLe
                                                                                                                                      194 sSerValGlyValIleAspLeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLy
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University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
                                                                                                                                                                                                                                                                                                                                                                                                                          234 uValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeu 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
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COMMENT Contact: Harrison MJ Plant Blology Division The Samuel Roble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7380 Email: mjharrison@noble.org Insert Length: 658 Std Error: 0.00 Plate: 038 row: F column: 11 Seq primer: TCACACAGGAAACAGCTATGAC. FEATURES SOURCE 1658	/organism="Medicago truncatula"  /mol_type="mann"  /db xref="texton:3880"  /clone="NF038F11PL"  /tissue type="teaf"  /dev stage="teaf"  /dev stage="teaf"  /dore lib="Phosphate starved leaf"  /note="Vector: Lambda Zap; At the trifoliate stage, M.  runcatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day  period, the plants were fertilized twice weekly with 1/2  Hoaglands solution containing only 20uM potassium  phosphate. RNA was prepared from above ground tissues."	310	Qy 88 ProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLySerLeuIleProLeu 107	euleuasnGlyAspAlaAlaGluLysIleLeuGlnAla 	18 31 37 22 24 24	Db 436 GARTCCATACATTAACATGAACTTCAAGGAAAAAAAAATATGATCCTAAGT 495  Qy 248 TyrleuargPheGlyLysGlualaThrargAlaGlnValleuasnAlaThrasnGlySer 267  Db 496 TACTTACACTTTGGTAGAAACCATCTCGAGCAGAATTTTGAAGGTCACATATTTT 555
Query Match:         37.08%         Indels:         0           DB:         Gaps:         0           US-09-657-631-4 (1-459)         X BQ255419 (1-735)         0           QY         1 GlnIleLysAsmMetGluPheLeulleThrLeulleAlaThrPheLeuLeuLeuMet         20           Exalt TAAGATTATGGAGTTCCTAATTACACTAATCACCACTGTTCTACTGTTAATG         120           QY         21 ProAlaIleThrSerSerGlnTyrLeuGlyAsnAsmAsmLeuleuThrAsmArgLysIlePhe         40           QY         21 ProAlaIleThrSerSerGlnTyrLeuGlyAsnAsmAsmArgLysTlaPhe         40           Dh         121 CrtGCAATCACTACACAAACAACAACTAATCAATAATTACAACA	4 GlnLysGinGluThrLeuThrSerTyrAlaVallePheAspAlaGlySerThrGlyThr  4 GlnLysGinGluThrLeuThrSerTyrAlaVallePheAspAlaGlySerThrGlyThr  181 CAAAACAATTCTCTCTTTTGCTGTGGTGTTTGGTGGTAGCACTGGTAGC  61 ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIlG  61 ArgValHisValTyrHisPheAspGlyBanCattTGTTCTTCTTCTTCATATTGGCAAGATGTT  81 GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla  1	OY 101 AlalysSerLeulleProLeuLeuGludluAlaGluAspValValProGluAspLeuHis 120	Qy         161 GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThr         180           Db         541 CAACCTGATGCAGTTATTATTGATGGAACCCAAGAAGGTTCTTATCTCTGGGTGACA         600           Qy         181 VALASHTYTVAlLeuGlyAsnLeuGlyLySSerPheThrIySSerValGlyVallleAsp         200           Db         601 GTTAACTATGCATTNNNGAAANANAGGGAAAAAGTACACAAAAACAGTGGGAGTAATGGAT         660	Oy 201 LeuGlyGlyGlyGloserValGlnMetThrTyzalaValSerLysLysThralaLysAsnala 220	RESULT 7 B1263104 LOCUS B1263104 CLOCUS DEFINITION NF038F11PL1F1095 Phosphate starved leaf Medicago truncatula cDNA CLOCUS ACCESSION B1263104 B1263	Medicago: Medicago: AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.K., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. TILLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library

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300 254

SOURCE ORGANISM

AUTHORS

TITLE

REFERENCE

JOURNAL

COMMENT

LOCUS

RESULT 8 BI270380

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a

ACCESSION

VERSION KEYWORDS

274

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AW584590 657 bp mRNA linear EST 07-SEP-2000 N210666e MHAM Medicago truncatula/Glomus versiforme mixed BST library cDNA clone MHAM-2Pl1, mRNA sequence.
                                                                                             61 AGAAGTACCTTCAATGTTCAACCTGATGCAGTTTCTATTATTGATGGAACCCAAGAAGGT 120
                                                                ArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGly 174
                                                                                                                                             SerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLys 194
                                                                                                                                                                    CysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGlyGlySerGlyGln 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula/Glomus versiforme mixed EST library Medicago truncatula/Glomus versiforme mixed EST library Eukaryota; mixed EST libraries.

1 (Bases 1 to 657)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D. Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M. ESTS from roots of Medicago truncatula after colonization with
    195 ServalGlyvalIleAspLeuGlyGlyGlyServalGlnMetThrTyrAlaValSerLys
                                                                                                                                                                                                                                                   215 LysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeu
                                                                                                                                                                                                                                                                                                                                241 TATACAGCTAAAAATGCTCCAAAAGTTGCTGATGGAGAAGATCCATACATTAAGAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                       ValleuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 AlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlySerAsnPheAspAspCysLysGluIleIleLeuLysValLeuLysValAsnAspPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 LysLysLeuPheValThrSerAlaPheAlaTyrLeuAlaGluAspValGly 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW584590.1 GI:7261644
                                                                                                                                                                                                                                               <u>:</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 580-221-7380
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VERSION
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COMMENT
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AW584590
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SOURCE
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//issue type="Developing flowers"
//dev_stage="Developing flowers"
//dev_stage="Developing, fully-opened flowers and flowers
in early transition into pods."
//clone_lib="Developing, fully-opened flowers and flowers
in early transition into pods."
//clone_lib="Developing, fully-opened flowers and flowers transitioning into pods. The cDNA was prepared flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the digapack III Gold packaging extracts. Phagemids containing cDNA inserts were using extasts. Phagemids containing cDNA inserts were using exAssist helper phage and the E. coli strain
XLI-Blue WRRY (Stratagene). Excised plasmids were plated using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                  Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
                                                                                                                                                                                     NF010D11FL1F1094 Developing flower Medicago truncatula cDNA clone NF010D11FL 5', mRNA sequence.
                                           615
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
268 AlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyr 287
                    556 CCCAACCTTGCATTTTAGCTGGATTTGATGGGACATACACATATGCTGGANAANAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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299
009
009
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
T=1: 580 221 7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Medicago truncatula"
                                                                                               Email: gdmay@noble.org
Insert Length: 652 Std Error: 0.00
Plate: 010 row: D column: 11
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                           LysAlaPheSerProSerSerGlySerAsnPhe
                                                                                                                                                                                                                                                                                                                    Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                   BI270380.1 GI:14877916
EST.
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869.00
86.64%
73.27%
36.45%
                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago.
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                                                                           288
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source

FEATURES

651

Other name: MHAM-2c-H06; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'. Location/Qualifiers 1. .657 FEATURES

135 LeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsn 154

Query Match: DB:

à

. No.:

Pred.

ORIGIN

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/tissue type="Developing flowers"
/dev_stage="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."
/clone lib="Developing flower"
/clone lib="Developing flower"
/note="Vector: Lambda Zap; cDNA was prepared from polyA-enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the B. coli strain XLI-Blue MRR* (Stratagene). Excised plasmids were plated using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                       Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library Unpublished (2001)
                                                                                                                            BQ148414 673 bp mRNA linear EST 24-APR-2002
NF068A12FL1F1097 Developing flower Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                           Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids 1, Fabales, Fabaceae, Papilionoideae, Trifolleae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 IleThrSerSerGlnTyrLeuGlyAsnAsn---LeuLeuThrAsnArgLysIlePheGln 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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168
22
24
24
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
TH: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 500 acr.
Bmail: gdmay@noble.org
Insert Length: 673 Std Error: 0.00
Plate: 068 row: A column: 12
Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                              NF068A12FL 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="NF068A12FL"
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87.96%
77.78%
35.82%
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1 (bases 1 to 673)
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Best Local Similarity:
Query Match:
DB:
                                          657
201
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                                                                                                                                                           DEFINITION
                                                                                        RESULT 10
BQ148414
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                                                                                                                                                      /dev stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
/lab host="E. coll strain XLOLR"
/lone lib="WHAM"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/hote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cNNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glowus versiforme. The cDNA was directionally lighted into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells:"
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'organism="Medicago truncatula/Glomus versiforme mixed EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlalysSerLeuileProLeuleuGluGluAlaGluAspValValProGluAspLeuHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnLysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 TCTGAAAAGATATTGCAAGGGTAAGGGATATGTTCAGCAATAGAAGTACCTTCAATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnIleLysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMet
                                                                                                                                       tissue_type="roots colonized with Glomus versiforme"
                                               | mol_type="mRNA"
|cultivar="Medicago truncatula genotype A17"
| db xref="taxon:119092"
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/db_xref="kaxon:3880"
/clone="RR091F05FL"
/tissue_type="Developing flowers"
/tissue_type="Developing flowers"
/dev stage="Developing, fully-opened flowers and flowers
in early transition into pods."
/clone_lib="Developing flower"
/clone_lib="Developing flower"
/clone_lib="Developing flower"
/note="Vector: Lambda Zap; cDNA was prepared from polyA+
enriched, pooled samples of equivalent amounts of total
RNA from very young, developing, fully-opened flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
using ExAssist helper phage and the B. coli strain
XLI-Blue MRF' (Stratagene). Excised plasmids were plated
using SOLR cells."
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Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
Unpublished (2001)
          ATTICITACICCCAATATCTIGGAAACAACATATTACTCACTAACCGTAAGATTTICCCA 145
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                 61
                                                                                                            ValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu 81
                                                              206 GTCCATGITTACCATITTGATCAAAACTIAAAICTICTTCATGITGGTAAAGAIGTIGAG
                                                                                                                                                                             82 PheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAla
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                                        LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: gdmay@noble.org
Insert Length: 625 Std Brror: 0.00
Plate: 091 row: F column: 05
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OX
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
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                                                                                                                                 95 AspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeuGluGluAlaGluAspVal
                                                                                                                                                 115 ValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArg
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Mismatches:
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88 ProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeu
                /organism="Medicago truncatula"
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Insert Length: 656 Std Brror: 0.0
Plate: 093 row: B column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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/db_xref="taxon:3880"
/clone="NF093B10IN"
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                                                                                                                                                                                                                                       Interval.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Radicago truncatula insect herbivory library

Unpublished (2000)

Unversity of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 5191

Email: kkorth@comp.uark.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="local and systemic leaves"
/dev_stage="mature"
/dev_stage="mature"
/clone lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 TATCTTGGAAACAATATACTCACCAATCGTAAAATATTTCCAAAACAAGAAACTCTAAAC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerTyralaValilePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPhe 67
                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids I; Fabales, Fabaceae; Papilionoideae; Trifolleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
                                                      B1265005
NF004G10IN1F1084 Insect herbivory Medicago truncatula CDNA clone
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163
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: kkorth@comp.uark.edu
Insert Length: 664 Std Brror: 0.0
Plate: 004 row: 6 column: 10
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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                                                                                                                                                    Medicago truncatula (barrel medic)
Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:3880"
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                                                                                           NF004G10IN 5', mRNA sequence.
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                                                                                                          BI265005
BI265005.1 GI:14867791
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842.50
86.04%
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35.34%
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Best Local Similarity:
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DB:
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SOURCE
ORGANISM
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VERSION
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BI265005
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/tissue type="local and systemic leaves"
/dev_stage="mature"
/dev_stage="mature"
/clone libr=Insect herbivory"
/note="vector: lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    656 bp mRNA linear EST 18-JUL-2001
NF093B10IN1F1089 Insect herbivory Medicago truncatula cDNA clone
NF093B10IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                              188 LeuglyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGln 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGlu 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599 ATGCTATATGCAGTCTCAGAGAACAAGCAAAAAAAAGCTNCACAAGTACCTCAGGGAGAN 658
127
                                                                                                         147
                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                 478
                                                                                                                                                                                                                                                                                                                  168 IleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsn 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 656)

Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,

Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula insect herbivory library

Unpublished (2000)
                                                                                                                                       128 GlyalaThralaGlyLeuargLeuLeuAsnGlyAspalaAlaGluLysileLeuGlnAla
                                                                                                                                                                                                            148 ThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIle
                                                                                                                                                                                                                                                        108 LeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrProLeuArgLeu
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Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
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PhevalAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 IleThrSerSerGlnTyrLeuGlyAsnAsn---LeuLeuThrAsnArgLysIlePheGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AAGAATATGATGAACTTTATGACACTCATC---ACATTTCTTCTTCTTCATTATGCCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 LysGlnGluThrLeuThrSerTyrAlaValllePheAspAlaGlySerThrGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ValHisValTyzHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAsplleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 TITIAIAATAAGACAACGCCCGGTITGAGTGCATACGCGGATAATCCAGAAGAAGAAGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysSerLeuIleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 GICCAIGITIACCAITITGAICAAAACITAAAICITCITCAIGITGGIAAAGAIGITGA
                   He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A.,
Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and
Dixon,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                    Email: radixon@noble.org
Medicago Genome Initiative accession: MGI:S:16915
Insert Length: 660 Std Brror: 0.00
Plate: 055 row: F column: 11
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660
165
22
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                                                                                                                                                                   2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
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Mismatches:
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Plant Biology Division
The Samuel Roberts Noble Foundation
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="stem"
                                                                                                                                                                                                                                                                                                                                                                                                /clone="NF055F11ST"
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     REFERENCE
                   AUTHORS
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Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                                                      201 GTCCATGTTACCATTTTGATCAAACTTAAATCTTCTTCATGTTGGTAAAGATGTTGGG 260
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                    LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAla
                                                                                                                                                                                                                                                                                                                                                                                     LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg
                                                                                                                                                                                                                                                                                   24 AAGAATATGARGARTTATGACACTICATC---ACALTITCTTCTTCATTATGCCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 CCTGATGCAGTTTCTATTATTGATGGAACCCAAGAAGGTTCTTATCTCTGGGTGACAGTT
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Matches:
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Mismatches:
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BE325702.1 GI:9199479
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Best Local Similarity:
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BE325702
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ProAsnLysProAsnSerIle---LeuHisProValAspPheGluIleGluAlaLysArg 373
                                                                                                                                                                                                                                                                                                                                                                              CysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGlyGerGlyGln 334
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195 ServalGlyValIleAspLeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLys
                                                                                                                                          ValleuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGlu
                                                                                                                                                                255 AlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro
                    67 ACAGTGGGAGTAATGGATCTTGGAGGTGGATCAGTTCAAATGGCATATGCAGTGTGCAAG
                                                                        InsthralaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeu
                                                                                         GlypheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer
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/dev_stage="trifoliate"
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/dev_stage="trifoliate"
/done_lib="phosphate starved leaf"
/note="vector: Lambda Zap; At the trifoliate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM poteassium
phosphate. RNA was prepared from above ground tissues."
                                                                                                                                                                                                                                                            EST 19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                       Medicago truncatula
bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Trifolieae;
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Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
                                                                                                                                                                                                                                                            BG457472 (659 bp mRNA linear EST 19-MAR-20
NF106A03FLIF1019 Phosphate starved leaf Medicago truncatula CDNA
clone NF106A03PL 5', mRNA sequence.
BG457472
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                            504 CCTGATGCAGTTTCTATTATTGATGGAACCCAAGAAGGTTCTTATCTCTGGGTGACAGTT
       ArgaspalavalSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
                                                                                                                564 AACTATGCATTGGGGAAATTGGGAAAAAATTCACAAAAACAGTGGGAGTAATGGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
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Mismatches:
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                                                                                                                                                       202 GlyGlyGlySerValGlnMetThrTyrAlaValSer
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Matches:
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GENERAL INFORMATION:
APPLICANT: Etzler, Marilynn E.
APPLICANT: Marphy, Judith B.
APPLICANT: Marphy, Judith B.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: U$\0.099129,112
PRIOR PLILNG DATE: 1998-08-04
PRIOR APPLICATION NUMBER: U$\0.089907,226
NUMBER OF SEQ ID NOS: 19
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US-09-370-265-6

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US-09-557-800C-4

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OTHER INFORMATION: full length clone
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OTHER INFORMATION: NBP46
NAME/KEY: modified base
LOCATION: (1)...(1458)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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st Local S: ery Match: -09-657-63: 2 2 2 4 4 4 4 12 12 18 8 8	Leuhis	Db 541 GTTAACTATGGGAATTTGGGAAAAGCTTCACAAATCAGTGGGAGTAATTGAC 600  Qy 201 LeuGlyGlyGerValGlnMetThrTytalaValSerLystysThrAlaLysAsnAla 220  Db 601 CTTGGAGGTGGTTCAATTGAATTGCAGTGTCAAAAAAACAGCAAAAAATGCT 660  Qy 221 ProLysValAlaAspGlyGluAspProTytIleLysLysLeuValLeuLysGlyLysGln 240  E	281 841 301 901 321

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LOCATION: (195)..(1436)
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aaaatcaggaaccagttacatcagtgatgctgttatatttgatgctggtagcactggaagc
                                                                                                                          ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle
                                          AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal
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Patent No. 6465716

Patent No. 6465710:

APPLICANT: Etzler, Marilynn E.

APPLICANT: Murphy, Judith B.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots

FILE REFRENCE: 025070-079810US

FILE REPRENCE: 192070-079810US

CURRENT APPLICATION NUMBER: US/09/129,112

CURRENT FILING DATE: 1998-08-08

PRIOR PILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATENTIN OF SEQ ID NOS: 19
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                                       GluLysileLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
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                                                                                                                                                                                                                                                            LysvalalaaspGlyGluaspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr
442 AlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
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US-09-129-112-18
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APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
PRIOR FILING DATE: 1998-08-04
PRIOR PILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene involved in oligosaccharide signaling
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OTHER INFORMATION: DBX9-for/rev primer
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OTHER INFORMATION: DBX2-for/rev primer NAME/KEY: primer bind LOCATION: Complement ((766). (785))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (297)...(314)
OTHER INFORMATION: DBX7-for/rev primer
NAME/KEY: primer_bind
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OTHER INFORMATION: DBX1-for/rev primer NAME/KEY: primer_bind.
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OTHER INFORMATION: DBXbottom primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer_bind
LOCATION: Complement((1)..(22))
OTHER INFORMATION: DBXtop primer
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OTHER INFORMATION: DBX12 primer
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LOCATION: (1071)..(1072)
OTHER INFORMATION: splice site
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OTHER INFORMATION: DBX4 primer
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OTHER INFORMATION: splice site
NAME/KEY: primer_bind
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 1434
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OTHER INFORMATION: DBX
NAME/KEY: sig_peptide
LOCATION: //
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LOCATION: (856)..(857)
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LOCATION: (61) .. (1404)
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LOCATION: (1133)..(11
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Alignment Scores:

Sequence 18, Application US/09129112 Patent No. 6465716 GENERAL INFORMATION: APPLICANT: Etzler, Marilynn E. us-09-657-631-4.p2n.rni

Qy 314 ProcysProTyrProSerCy	Db 1024 GARACAACTITITIGITIC  QY 354 GLUPLOASHLYSPROASHGC :::	Oy 374 AlaCysAlaLeuAsnPheGl	2y 394 ArgProTyrValCysMetAs        :::      1204 GITCCTIACAIAIGITIGGA	Qy 414 LeuGlybroArgLysGlull :::       Db 1264 ATTGATCCCCAGCAAGAGAT	Oy 434 GlualaalaTrpProLeuGl	Qy 454 ArgLeuMetTyrPheile 4 :::           ::: Db 1384 AAATTAATGTATTCCTT 1	RESULT 5 10-09-129-112-3 5 Sequence 3, Application US/09129 7 Patent No. 6465716	GENERAL IN APPLICANT APPLICANT APPLICANT	; TITLE OF INVENTION: A No. 64657; ; FILE REFERENCE: 023070-0798HOUS; ; CURRENT APPLICATION NUMBER: US/, ; CURRENT FILING DATE: 1998-08-0	PRIOR APPLICATION NUMB PRIOR FILING DATE: 199 NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn Ver	3 6265 A : Dolichos bifl	; FEATURE: ; OTHER INFORMATION: genomic seq.; NAME/KEY: exon ; LOCATION: (633)(944)		intron (1152)(15 exon (1560)(16	KEY: ION: KEY: ION:	US-09-129-112-3 Alignment Scores: 2.57e-112 Score: 998.50
Pred. No.: 1.52e-163 Length: 1434 Score: 1403.00 Matches: 263 Percent Similarity: 74.89% Conservative: 86 Best Local Similarity: 56.44% Mismatches: 107 Query Match: 58.85% Indels: 10 DB: 4 Gans. 3	(1-1434)  1ThrPheLeuLeuLeuLeuMetProAlaile	24 Thr     64 ACTGCAA	TCCTCCGATAATAATATTCGATTGAAGAAACCATTAATATCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCGATTATTCTTTTATTCTTTATTCTTTTATTCTTTTATTCTTTTATTCTTTTATTCTTTATTCTTTATTCTTTTATTCTTTTATTCTTTTATTCTTATTCTTTATTA		Oy 74 LeuHisIleGlyAsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaryr 93 Db 244 CTTCGCATGGCCATGAGCTGTCGTCAAGACGAAGCCAGGTTAAGTGCATAC 303		Oy 114 ValvalProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeu 133	Qy 134 ArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSer 153	Oy 154 AsnargSerThrLeuAsnValGlnArgAspalaValSerIleIleAspGlyThrGlnGlu 173  Db 484 AAGAGAAGCACTTGAAGGTTGAGGCGATGCAGTTTCAGTGTGAAAACCAAGAA 543	Oy 174 GlyserTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThr 193    :::	Qy 194 LysSerValGlyVallleAspLeuGlyGlySerValGlnMetThrTyrAlaValSer 213	Oy 214 LysLysThralaLysAsnalaProLysValalaAspGlyGluAspProTyrIleLysLys 233 :::::	Oy 234 Leuvalleulysglylysglnfyraspleutyrvalhissertyrleuargpheglylys 253 :::	Qy 254 GlualaThrargalaGlnValLeuasnalaThrasnGlySeralaAsnProCys1leLeu 273 	Qy 274 ProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSer 293	Oy 294 SerGlySerAsnPheAspAspCysLysGlullelleLeuLysValLeuLysValAsnAsp 313

314		1084	Qy 374 AlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArgLeuThrAspAlaLys 393	Qy 394 ArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeuValHisGlyPheGly 413	Qy 414 LeuGlyProArgLysGlulleThrValGlyGluGlyIleGlnTyrGlnAsnSerValVal 433 :::	Qy 434 GluhlaAlaTrpProLeuGlyThrAlaValGluhlaIleSerAlaLeuProLysPheLys 453	Cy 454 ArgLeuMetTyrPhelle 459	RESULT 5 US-09-129-112-3 ; Sequence 3, Application US/09129112 ; Patent No. 6465716	; GENERAL INFORMATION: ; APPLICANT: Bt2ler, Marilynn B. ; APPLICANT: Murphy, Judith B. ; APPLICANT: The Regents of the University of California	TITLE OF INVENTION: A No. 6465716 Factor Binding Prote FILE REFERENCE: 023070-079810US CURRENT APPLICATION NUMBER: US/09/129,112 CURRENT FILLING DATE: 1998-08-04		; SEQ ID NO 3 ; LENGTH: 6265 ; TYPE: DNA ; ORGANISM: Dolichos biflorus	; FEATURE: ; OTHER INFORMATION: genomic sequence of NBP46 (DB46) ; NAME/KEY: exon ; LOCATION: (633)(944)	NAME/KEY: : LOCATION: NAME/KEY: 6 LOCATION:	intron (1152) exon (1560)	; NAME/KEY: intron ; LOCATION: (1617)(1697) ; NAME/KEY: exon ; LOCATION: (1698)(1790) US-09-129-112-3	Alignment Scores: 2.57e-112 Length: 6265 Pred. No.: 2.57e-112 Matches: 307
1.52e-163 Length: 1434 1403.00 Matches: 263 74.89\$ Conservative: 86 56.44\$ Mismatches: 107 58.85\$ Indels: 3	) x US-09-129-112-18 (1-1434)	uPheLeulleThrLeulleAlaThrPheLeuLeuLeuLeuMetProAlaile 23 	SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIle 39        :::       :TGCAAGTTCCTTTTCCCTCCATGGGAGGGCTTCAAGCATCGCAAGTTTTCC 123					oGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeu 133  ::::::             TCAAGAGTTGCATCCCGAACACCCGTTAAAGTTGGAGCAACCGCAGGTTTA 423	uAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSer 153 	rThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGlu 173 	rMetrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysserPheThr 193 	IGIYValIleAspLeuGlyGlyGlyGlySerValGlnMetThrTyrAlaValSer 213 	rAlaLysaAsnalaProLysValalaAspGlyGluAspProTyrIleLysLys 233 	ulysglylysglnfyraspleutyrvalHissertyrleuargpheglylys 253  :::       :::    CAGGGAAAAATAITACCTCTATGTACACAGTTACTTGCGTTATGGTTTG 783	ArgalaGinValleuAsnalaThrAsnGiySerAlaAsnProCysileLeu 273        :::         CGIGCAGAGGITTTAAAGGITTCTCGTGATTCAGAAAACCTTGTATTTTG 843	eAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSer 293  :::   :::	rankneaspaspyslysglullelleleulysvalkendspas 313  -::     -::

1653 ACTACGCTTTCAATGTCTTAACTTTCGTTTTCTCTCATGTTGAAGGTTAGGGAAATGTTC 1712 153 SerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGln 172             ::    ::	173 GluGlySerTyrMetTrpVal	1832 AATTTTTTACTTAAGAAGATGGAAGAAGTGTGATCACATTACCTAGGACALTCATCTT 1891	17911892 AITTAAAAATAATTAATAATAATAATTAATTAAATTAGAATTGGTAT 1951	AITGIGAAAAAGAAAAGIAGAITGAITITTCAITAIGGIAAAGIAITITIAAIAAAITITI	ATTAACTCTTTTTAACTTTTAAAAATATAGGATCACTTTATGTGTGTG	TACCCCATATGGACAATTACTGACATGCCATACCGGATATATTAATATTTATCAATTGT	2132 CAATTTATTGTAACTACTTTAAAAATACTTTTAATTAAATGAGTGTGTGCT 2191	2192 TIAGTITITITITAAATICGAAAAATAATIAATAATIATIAGATATACTGGAAGAATIT 2251	2252 CCGAAGGATATTCATATCATATATATCTTGTAAGATAACATTTTTTTT	2312 AACACTATCTCTAAATATGATTTTTTTTTTTATGTCGAATGAAT	2372 IGIATAAGTAATTAAATTCACTATTCATTTTTATTTGTTGTTGTTTTTAGGGTCCGCC 2431	2432 AATTAGCTAAATCTTACCTAAAAAGATTGCAAACAAAGAAAAAAAA	AAATTAAAAGTGGATCAAACCATGAGGATATGTTTCAAAAAGAAGAATTAGGTTCTTTGT	179 L79 2552 TAIGTTTCAAAAACTAGTAGTTGGAATTTCTTAAATTCAATTATAATTAAT	TIGICIGCITAAITGATAATATAAAATAGCATAACIGATACATTTATAAATTATATT	2672 TATTAAAATTTATTTTTATTATAGATAAAATGTATTTGGTAATATTTATAATA
d Qy	od o	Db 52	à a ∂	ž 8 c	전 전 ·	S 6 5	<del>}</del> 8 ₹	3 8 8	3 음 8	් සි රි	ୁ ଶ ବ		oy da	දු සි දි	77 qq .	8 8 8
Similarity: 23.91% Conservat cal Similarity: 19.37% Mismarche atch: 41.88% Indels:	-657-631-4 (1-459) x US-09-129-112-3 (1-6265) 3 LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuMetLeuMetProAla 22	23 IleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLys1lePheGln 41	42 LysglnGluThrLeuThrSerTyralaValIlePheAspAlaGlySerThrGlyThrArg 61 	62 ValHisValTyzHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu 81	82 PheValAspLys	86	96 AsnprogludinalaalaLysSerLeuIleProLeuLeuGludlualadluAspValVal 115 	116 ProgluAspLeuHisProLysThrProLeuArgLeuGly 128        :::	128	128	128 128 1293 TAATAATATAAAATGAATATGAAACTAATATTCTGATGGAAGAAGAAAGA	128 128 1353 AAGAGACAAAACACACTTTGATGAGCTCTATCTTTAAACAAAAAATGGAATTGAA 1412	128 128 1413 AGACCAAATAAAATAGGCATTAGCCCATATCATAAAATCTTTTGTAAAATATTAATAGAA 1472		129	140 AlaAlaGluLySIleLeuGlnAla

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886 GGGGAGGTGGGCTTTGAGCCCTGCTATGCCGAAGTGCTGAGGGTGGTACGAGGAAAACTT 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      706 AAGCICIAIACACAIAGIIACCIGGGAIIIGGAIIGAAAGCIGCAAGACIAGCAACCCIG 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 AsnAla-----ThrAsnGlySer------AlaAsnProCysIleLeuPro 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glyser---AsnPheAspAspCysLysGluIleIleLeuLysValLeu-----LysVal 311
                                                                                                                                                                                                                                                                                                                                                                                                                                         ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 TTTGATTCTGTGAAGCCAGGACTTTCTGCTTTTGTAGATCAACTAAGCAGGGTGCTGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
                                                                                                                                                                                                                                                                                                                                                                                                      TTGTGCAGAAAATGCCAGGACAGCTTCCAATTCTA-----GAAGGGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeulleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 LyslleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 AspAlavalSerileIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn
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Mismatches:
Indels:
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                                                                                                                           Length:
Matches:
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507.50
49.41%
33.97%
21.29%
               FEATURE:

, NAME/KEY: CDS

, LOCATION: (1)..(1284)

US-09-608-285A-4
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Query Match:
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ORGANISM: Homo
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APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Foung, George
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION NUMBER: US/09/608,285A
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-00-25
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-07-16
PRIOR PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
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Patent No. 6335013
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307 ACCGTICAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGAAAAG
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APPLICANT: Ford, John
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/35761
CURRENT APPLICATION NUMBER: U5/09/350,836B
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR PLING DATE: 1999-07-16
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-24
PRIOR PLING DATE: 1999-02-04
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                                            SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----AlaGlu
                                                                                                       349 AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu
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Conservative:
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Length:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-350-836B-4
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307 ACCGITCAAGGGCTCITAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGAAAAAG 366
                                                                                          143 LysileLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
                                                                                                             106 AAGCICIATACACATAGTIACCIGGGATITGGATIGAAAGCIGCAAGACTAGCAACCCTG
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        ---GGCAGTCCTTTCCTGTGCATGGATCTCAGCTACATCACAGCCCTGTTA 1161
                                                                                                  GlnasnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla 448
                                     409 ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr 428
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APPLICANT: FORGA, John
APPLICANT: FORGA, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REPERENCE: 28111/35908
CURRENT PAPLICATION NUMBER: US/09/370,265
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER APPLICATION NUMBER: DC1/US99/16180
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-02-09/122,444
EARLIER FILING DATE: 1999-02-09/122,449
EARLIER FILING DATE: 1999-02-09/122,449
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-24
EARLIER FILING DATE: 1998-07-26
EARLIER PILING DATE: 1998-07-16
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Matches:
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Patent No. 6447771
GENERAL INFORMATION:
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GCTCTGCTCTTTGAGGTAAAGGAGATCTTC---AGGAAGTCACCTTTCCTGGTACCAAAG 483
                                                                                                                                           TITCTGACAGGTCAGCTGCATGGCCACAGACAGAGACTGTGGGGACCTTGGACCTAGGG 603
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                                 163 AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn
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946 CACCAGCCAGAGGACGTCCAGAGGTTCCTTC-------
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APPLICANT: Ford, John APPLICANT: Mulero, Julio
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                                                                                                                                                       TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-00-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-24
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                                             Sequence 4, Application US/09557800C
Patent No. 6476211
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SEQ ID NO 4
LENGTH: 1287
                                                                               GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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Best Local Similarity:
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; LOCATION: (1)
US-09-557-800C-4
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706 AAGCTCTATACACATAGTFACCTGGGATTTGGATTGAAAGCTGCAAGACTAGCAACCCTG 765
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APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Weng, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 2810/3650
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
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PRIOR FILING DATE: 1999-07-09
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                                           262 AsnAla-----ThrAsnGlySer-
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         OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
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         TITLE OF INVENTION: METHODS AND MATERIALS RELIGIBLE REPERENCE: 28110/35908
CURRENT APPLICATION NUMBER: 05/09/370,625A
CURRENT FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHTIN VET: 2.0
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-370-625A-4
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                                           -AlaAsnProCyslleLeuPro 274
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APPLICANT: Ford, John
APPLICANT: Ford, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TILE REFERENCE: 28110/35761
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR PLING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR APPLICATION NUMBER: 09/12,449
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1998-07-24
PRIOR PLING DATE: 1999-02-04
PRIOR RELING DATE: 1999-02-04
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                                     262 AsnAla----ThrAsnGlySer-
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ORGANISM: Homo sapiens
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OGCANISM: Homo sapiens
COGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: (246)..(1529)
NAME/KEY: misc_feature
LOCATION: (1718)
COCATION: (1718)
COTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
US-09-608-285A-2
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Matches:
Conservative:
Mismatches:
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	349 AspvalGlyMetValGluProAsnLy 349 AspvalGlyMetValGluProAsnLy 1257 GACACAGACATGATTGATTATGAAAA 369 IleGluAlaLySAYGAlaCySAlaLe 369 IleGluAlaLySAYGAIGCYAAT—	389	Db 1359GGCAGTCCTTTCCTGTGCATGGATCTCAGTACATCACAGCCCTGTTA 1406 Ov 409 ValHisGlvPheGlyLeuGlyProArgLysGlulleThrValGlyGluGlyIleGlnTyr 428	1407	1458	1515 CTG	NE-09-370-265-2; Sequence 2, Application US/09370265; Sequence 2, Application US/09370265; Patent No. 6447771.	APPLICANT: FORM, John   APPLICANT: Mulero, Julio   APPLICANT: Mulero, Julio   TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE   TITLE OF INVENTION: POLYPEPTIDES	FILE REFERENCE: 28111/35908 ; CURRENT APPLICATION NUMBER: US/09/370,265 ; CURRENT FILING DATE: 1999-08-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0-0		FARLIER FILING DATE: 1999-03-19; EARLIER FILING DATE: 1999-03-04; EARLIER FILING DATE: 1999-02-04;	AFPLICATION NOMBER: 09/118,20 PILING DATE: 1998-07-24 APPLICATION NUMBER: 09/118,20 FILING DATE: 1998-07-16				; OTHER INFORMATION: n = adenine or guanine or cytosine or tnymine US-09-370-265-2	Alignment Scores: 2.14e-52 Length: 1799 Pred. No.: 507.50 Matches: 143
; LOCATION: (246)(1529) ; NAME/KEY: misc_feature ; LOCATION: (1718) ; OTHER INFORMATION: n = adenine or guanine or cytosine or thymine US-09-350-8358-2	Alignment Scores: 2.14e-52 Length: 1799 Pred. No.: 507.50 Matches: 143 Score: 65 Percent Similarity: 49.41% Conservative: 65 Best Local Similarity: 33.97% Mismatches: 152 Query Match: 4 Gaps: 16		Oy 47 ThrSerTyrAlaValilePheAspAlaGlySerThrGlyThrArgValHisValTyrHis 66	Oy 67 PheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82	Qy 83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102	Qy 103 SerLeuIleProLeuLeuGludluAlaGluAspValValProGluAspLeuHisProLys 122 :::::	Oy 123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuAsnGlyAspAlaAlaGlu 142	Oy 143 LysIleLeuGlnalaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162 :::	Qy 163 AspalaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182 	OY 183 TYRValLeuGlyAsnLeuGlyLySSerPheThrLySSerValGlyValIleAspLeuGly 202	Qy 203 GlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro 221	Qy 222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241 :::	Qy 242 AspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261	Oy 262 AsnalaThrasnGlySerAlaasnProCysIleLeuPro 274	Qy 275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294	295 GlySerAsnPheAspAspAspAsglulleIleIleLeuLysValLeuLysVal	A LE

Percent Similarity: 49.414 Minarity 21.234 Indels: 65  Obery March: 21.234 Indels: 61  Description: 4.124 Indels: 61  Substitution: 4.124 Indels: 61  Description: 6.124 Indels: 61  A 7 TheSerytralwallenbagoalachyserifficallymhargvalHisvally  A 7 TheSerytralwallenbagoalachyserifficantraferifficantraferifficantraferificantraferifficantraferif	tches: 65 tches: 152	OY 389 LeuThrAspAlaLysArgProTyrValCy		oLys 1      AAAG 6		728 ; APPLICANT: Yeung, George ; TITLE OF INVENTION: Methods and Materi 182 ; TITLE OF INVENTION: Polypeptides ; FILE REPERENCE: 28110/36457 ; CHRERNT REPERENCE: 28110/36457	LeuGly 202	221	241.	1	274 ; PRIOR FILING DATE: 274 ; NUMBER OF SEQ ID R 5 SOFTWARE: PatentII 1070 ; SEQ ID NO 2	294 ;	311	1223 Alignment Scores:	GIL
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                                                                                                                                PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe
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                                                                                       1406
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                                                                                                                                   409 ValHisGlyPheGlyLeuGlyProArgLySGluIleThrValGlyGluGlyIleGlnTyr
                                                                                                                                                                  1407 AAGGATGGCTTTGCA------GACAGACAGTCTTACAGCTCACAAAGAAA
                                                                                                                                                                                                                            429 GlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla
                                                                 LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu
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DAME/KEY: CDS
LOCATION: (246)..(1529)
FEATURE:
NORME/KEY: misc_feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: POTATION
APPLICANT: MULECO, JULIO
APPLICANT: MULECO, JULIO
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD35
FILE REPERENCE: 2011/035908
CURRENT APPLICATION NUMBER: US/09/370,625A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PGT/US99/16180
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
SOFTWARE: PARENTING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PARENTIN Ver. 2.0
SEQ ID NO 2.
1314 AGAAAAGCCAGGGAAGIGIGIGAI---AACTIGGAAAACTICACCICA-
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09370625A; Patent No. 6600032; GENERAL INFORMATION:
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	123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142        ::	143 LyslieLeuglnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162	163 AspalavalSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182 		22			274	275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294 :::        ::    ::   1071 TGGTTGGAAGTGGATCTTTGGGGGTGTGAATACGGTTGGTGAATAATACAGTAATAGGTGGAACTAAGAA 1130	311		PhealaryxLeuAlaglu 34	36	38	alcysmetAspLeuLeuTyrGlnHisValLeuLeu 40 ::                TGTGCATGGATCTCAGCTACATCACAGCCCTGTTA 14	409 ValHisGlyPheGlyPeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr 428	GlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla     ::: :::      GTGAACAACATAGAGACGGGCTGGGGCCTTTGGGGGCCACCTTTCACCTGTTGCAGTCT	449 Leu 449
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Db 1515 CTG 1517

Search completed: August 19, 2004, 20:35:42 Job time : 114.192 secs This Page Blank (uspto)

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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APPLICANT: Etzler, Marilynn E.
APPLICANT: Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US2002019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-0798100S
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR PILING DATE: 1997-08-06
RNOMER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
        Sequence 8, Appli
Sequence 13, Appl
Sequence 1, Appli
Sequence 8688, Appli
Sequence 2234, Appli
Sequence 11084, Appli
Sequence 11084, Appli
                                                                                                                                                                                                                                                                                                                                 Sequence 73, Appl.
Sequence 285, Appl.
Sequence 30.991,
Sequence 6144, Appl.
Sequence 89910, A
Sequence 89910, A
Sequence 119497,
Sequence 52833, A
Sequence 5388, Appl.
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                                                                                                                                                                      Sequence 849, App
Sequence 849, App
Sequence 29868, A
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Sequence 1888, Ap
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1 US-09-938-842A-849

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1 US-09-938-842A-849

1 US-10-437-963-1908

2 US-10-425-114-1508

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3 US-10-425-114-1508

5 US-10-259-165-28

5 US-10-259-165-28

5 US-10-259-165-28

1 US-10-425-114-6144

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7 US-10-425-99-123779

2 US-10-425-114-6144

7 US-10-425-114-6144

7 US-10-425-114-6144

8 US-10-425-114-6144

8 US-10-424-599-123779

4 US-10-091-085-4

4 US-10-091-085-2

4 US-10-091-085-2

5 US-10-286-926-4

6 US-10-286-926-4

6 US-10-286-926-4

7 US-10-092-063-6

8 US-10-286-926-4

8 US-10-286-926-4

8 US-10-286-926-3
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      1544
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LOCATION: (1)..(1458)
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                    1665.5
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                                                                                         August 19, 2004, 15:09:55; Search time 616.984 Seconds (without alignments) 3654.341 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US10_NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                            nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        3228839 seqs, 2456066551 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       BLOSUM62
Kgapop 10.0 , Kgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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score greater than or equal to
and is derived by analysis of
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Maximum DB seq length: 200000000
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Match Length DB
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Jatabase

Description

Score

900

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Sequence 13, Application US/09129112
| Sequence 13, Application US/09129112
| Sequence 13, Application US/09129112
| Sequence 13, Application Sequence 13, Application Sequence 13, Application Sequence 13, Applicant Murphy, Judith B.
| APPLICANT: Murphy, Judith B.
| APPLICANT: The Regents of the University of California TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots FILE REFRENCE: 023070-079810US
| FILE REFRENCE: 023070-079810US
| CURRENT APPLICATION NUMBER: US/09/129,112 CURRENT FILING DATE: 1998-08-04
| PRIOR APPLICATION NUMBER: US 08/907,226
| PRIOR PILING DATE: 1997-08-06
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                   ThrValGlyGluGlyIleGlnTyrGlnAenSerValValGluAlaAlaTrpProLeuGly 440
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                                                                                                                                ThrPheGlyGlyIleTrpAsnGlyGlyGlyGerGlyGinLysLysLeuPheValThr 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThralaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
                                                                                                                                                                                                                                                                                            381 AspVallysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAsp
                        CystysGluIleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCys
                                                                                            361 IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu
781 TIGAAIGCAACTAAIGGAICTGCTAACCCIIGCAITITACCIGGAITIAAIGGGACCIII
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; OTHER INFORMATION: full lei; NAME/KRY: CDS
; LOCATION: (43)...(1413)
; OTHER INFORMATION: NBE46
US-09-129-112-13
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Best Local Similarity:
Query Match:
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NAME/KEY: CDS
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; Sequence 8688, Application US/20040034888A1
; Sequence 8688, Application No. US2004003488BA1
; Gublication No. US2004003488BA1
; Gublication No. US200400348BBA1
; APPLICANT: Liu, Jingdong
; APPLICANT: AD401, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53313) B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; EDG ID NO 8688
; EDG ID NO 8688
; EDG ID NO 8688
; EDG ID NO 8688
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17 AACATGAATTITCTA-----ACCTICGITACTGTICTIACTCATACTACCAGCAACC
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US-10-424-599-2234
                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 2234
LENGTH: 1532
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Best Local Similarity:
                                                                                                           TYPE: DNA
ORGANISM: Glycine
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                                 GlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLys
                                                                                                                           662 CCACCAGAAGGAGAAGAACATACATAAAGACTCTTGTACTTAATGGAAAAACTTATGAC
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                                                                                             TyrvalleuglyAsnLeuglyLysSerPheThrLysSerValGlyVallleAspLeuGly
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Publication No. US20040031072A1
GENERAL INFORMATION:
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124 TCCTCCGATAATAATTATTCGATTGAAGAACCATTAATGAATCTTATGCAGTTATCTTC 183
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Mismatches:
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Gaps:
            NAME/KEY: primer_bind
LOCATION: (297)...(314)
OTHER INFORMATION: DBX7-for/rev primer
NAME/KEY: primer_bind
LOCATION: (667)...(685)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ON: (1133)...(1151)
INFORMATION: DBX9-for/rev primer
                                                                      OTHER INFORMATION: DBX1-for/rev primer NAME/KEY: primer bind LOCATION: /fee* _'---
                                                                                                                                                LOCATION: (688)...(704)
OTHER INFORMATION: DBX2-for/rev primer
LOCATION: Complement (766)...(785))
OTHER INFORMATION: DBX10 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAME/KEY: misc_feature
LOCATION: (1071). (1072)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
LOCATION: Complement((1075)..(1093))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: DBXbottom primer US-09-112-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: DBX11 primer NAME/KEY: primer_bind LOCATION: (1133)..(1151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1227)...(1247)
OTHER INFORMATION: DEX12 primer
                                                                                                                                                                                                                                                       OTHER INFORMATION: splice site NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: DBX5 primer NAME/KEY: primer bind LOCATION: (933)...(952) OTHER INFORMATION: DBX3 primer NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (955)..(972)
OTHER INFORMATION: DBX4 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.29e-167
1403.00
74.89%
56.44%
58.85%
                                                                                                                                                                                                                                                                                                                                                      primer
                                                                                                                                                                                                                                                                                                                                 LOCATION: (857)...(872)
OTHER INFORMATION: DBX6
                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (856)..(857)
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer bind LOCATION: (878).. (896)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
LOCATION: (1227)..(12
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Best Local Similarity:
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DB:
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Factor to US20020019995A1
GENERAL INFORMATION:
APPLICANT: Erzler, Marilynn E.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots;
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PALENTING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
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| TATCAGTATACGTTGCTCGATGGATTTGGCCTGGATCCTTGGAAGAGATTATAGTA 1270
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TATCCTGCGGAATTCAAGGCCGCAGCTAAGCGAGGTCAAGTCAAATTTGAGGATGCT 1150
                                                                                                                                                                                                                                  GlyGly11eTrpAsnGlyGlyGlyGlySerGlyGlnLySLySLeuPheValThrSerAla 342
                                                                                                                                                                                                                                                                                                                                                                                           363 HisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspVal 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysserThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuLeu 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla 442
                                                                                                                                                                             PheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerlleLeu 362
                                                                        283 SerglyvalGluTyrLygAlaPheSerProSerSerGlySerAsnPheAspAspCysLys 302
                                                                                              850
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                    AlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyr
                                                                                                                                                        GluileileheulysvalleulysvalasnasprocysproTyrProSerCysThrPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene involved in oligosaccharide signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide
LOCATION: (61). (1404)
NAME/KEY: primer bind
LOCATION: Complement((1)..(22))
OTHER INFORMATION: DBXtop primer
NAME/KEY: primer bind
LOCATION: (274)..(291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Dolichos biflorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (1)...(1404)
OTHER INFORMATION: DBX
MAME/KEY: SIG_Deptide
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US-09-129-112-18
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US-10-425-114-11084

Sequence 11084, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Abou, Yihua

APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Pabaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Papaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 TCTTCTTCTTCCTCCTCTATCTTGGGAAGGGC---TTCTCCCCATCGCAAATTGTCTCCC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PheGlnLysGlnGluThrLeu---ThrSerTyrAlaValIlePheAspAlaGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ThrGlyThrArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThr
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Mismatches:
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Matches:
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                                                        1384 AAATTAATGTATTTCCTT 1401
                      454 ArgLeuMetTyrPhelle
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73.81%
55.19%
56.75%
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                                                                                                                                                                                                                              154 AsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGlu 173
                                                                                                                                                                                                                                                                                                GlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThr 193
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                             ArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSer
244 CTTCGCATTGGCCATGACCTTGAGCTGTTCGTCAAGACGAAGCCAGGTTTAAGTGCATAC
                                                                                                                 ValValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeu
                                                                                                                                                                                                                                                     LeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLys
                                                                                                                                                                                                                                                                                                                     LysSerValGlyValIleAspLeuGlyGlySerValGlnMetThrTyrAlaValSer
                                                                                                                                                                                                                                                                                                                                                                                               604 AAGACGGTTGCTGTTGACCTAGGTGGTGGTGGATCTGTTCAAATGGCTTACGCAATCTCA
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Mismatches:
Indels:
                                                                                                                                                                                                       MRT3847_49857C.
TITLE OF INVENTION: Plants and Uses Thereof: FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 87316
LENGTH: 1784
                                                                                                                                                                                                                                                                                      Length:
Matches:
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72.86%
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                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
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Query Match:
                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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; Sequence 87316, Application NS. US20040031072A1
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Applicant: Zhou Yihua
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; ITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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Retent No. US20020160378A1

Retent No. US20020160378A1

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Amage, Xun

APPLICANT: Amage, Xun

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APPLICANT: Amage, Xun

FILE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE PREFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

SEQ ID NO: 888 ID NOS: 5379

SEQ ID NO: 888 ID NOS: 5379

LENGTH: 1419
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                               GAGAAAGCAGCAAAGAAAGCTTGTAGTATGAAGCTGGAAAGAGGGAAAATCAACGTTCCCA
                                                                                                                                                                                                                       388 ArgLeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeu
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                                                                                                                                                   GlulleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro
         GlyGlyGlyGlySerGlyGlnLysLysLeuPheyalThrSerAlaPheAlaTyrLeuAla
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US-09-938-842A-1888
Sequence 1888, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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US-09-938-842A-1888
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LeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAla 268
                                           448 GCAACTGCAGGTTTGAGAGCTTTGGGTCACCAAGCCTCTGAAAACATTTTGCAAGCGGTT
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                                                                                                      ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIlelle
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Publication No. US20040009476A9
GENERAL INFORMATION:
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Sequence 849, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: BARES-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REPRESENCE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 5379

THOMBER OF SEQ ID NOS: 5379
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                                   1291 CTCATTGATGGATTCGGATTGGAGCCATCACAGACAATAACGTTAGTGAAGAGGGCCAA
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ORGANISM: Arabidopsis thaliana
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APPLICANT: La Kovalic, David K.
APPLICANT: La Kovalic, David K.
APPLICANT: La Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
SEQ ID NOS: 204966
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748 TCTTATGTCAGAGAAATGTATTTGAAGGGACGAAAGTATTTCCTCTATGTTCATAGCTAC
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                                               ProTyr11eLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr
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                APPLICANT: RAPELLAND RAPPLICANT: RAPPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 849
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Matches:
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ORGANISM: Arabidopsis thaliana
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US-09-938-842A-849
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ORGANISM: Zea mays
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                       US-09-657-631-4 (1-459) x US-10-437-963-29868 (1-2071)
                      OTHER INFORMATION: Clone ID: PAT_MRT4530_34328C.1
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ORGANISM: Oryza sativa
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                                  US-10-437-963-29868
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Sequence 1908 Application US/10425114
Sequence 1908 Application US/2044003488BA1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Acrem. Steven E
APPLICANT: Cao, Yongwei
TTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Matches:
Conservative:
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; OTHER INFORMATION: Clone ID: LIB3136-007-H10_FLI
US-10-425-114-19008
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Should, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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TATGCAGACACAGTTGGAGTAGTGGATCTTGGTGGTGGATCTGTCCAAATGGCATATGCT 586
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                                                                       IlePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAspGlnAsnLeu
                                                                                                                                    72 AspleuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysProGlyLeuSer
        32 AsnLeuLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeuThrSerTyrAlaVal
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209 ThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAsp
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